

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 25, 2005, 13:57:34 ; Search time 108.98 Seconds  
(without alignments)  
3741.440 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 4782  
Sequence: 1 MKTSLFWLVSSVLAFFSCHL.....MEIRGSSRNRYVDVTKLRF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_21.\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description         |
|------------|--------|-------------|--------|----|---------------------|
| 1          | 4782   | 100.0       | 928    | 2  | AAW88417 Chlamydia  |
| 2          | 4782   | 100.0       | 928    | 3  | AAAY90236 Chlamydia |
| 3          | 4782   | 100.0       | 928    | 5  | ABB90583 Chlamydia  |
| 4          | 4782   | 100.0       | 928    | 6  | ABU26757 Protein e  |
| 5          | 4774   | 99.8        | 949    | 2  | AAAY35060 Chlamydia |
| 6          | 1862   | 38.9        | 918    | 3  | AAAY69369 Amino aci |
| 7          | 1855   | 38.8        | 928    | 3  | AAAY94327 Chlamydia |
| 8          | 1853   | 38.7        | 928    | 2  | AAW88421 Chlamydia  |
| 9          | 1836   | 38.4        | 918    | 2  | AAW88422 Chlamydia  |
| 10         | 1802   | 37.7        | 926    | 5  | ABP56019 Chlamydia  |
| 11         | 1802   | 37.7        | 926    | 5  | ABB98228 Chlamydia  |
| 12         | 1802   | 37.7        | 926    | 6  | ABU6284 C. psitt    |
| 13         | 1794   | 37.5        | 928    | 5  | ABB90542 Chlamydia  |
| 14         | 1794   | 37.5        | 928    | 9  | ADW65028 C. pneumo  |
| 15         | 1793   | 37.5        | 928    | 2  | AAW88423 Chlamydia  |
| 16         | 1787   | 37.4        | 928    | 3  | AAAY90239 Chlamydia |
| 17         | 1785   | 37.3        | 928    | 2  | AAW88418 Chlamydia  |
| 18         | 1784   | 37.3        | 928    | 5  | ABB90573 Chlamydia  |
| 19         | 1763   | 36.9        | 930    | 2  | AAAY35052 Chlamydia |
| 20         | 1761   | 36.8        | 930    | 5  | ABB90548 Chlamydia  |
| 21         | 1761   | 36.8        | 930    | 6  | ABU26756 Protein e  |
| 22         | 1758.5 | 36.8        | 927    | 2  | AAAY35054 Chlamydia |
| 23         | 1757   | 36.7        | 928    | 3  | AAAY90237 Chlamydia |
| 24         | 1755   | 36.7        | 930    | 2  | AAW88424 Chlamydia  |

|    |        |      |     |   |                     |
|----|--------|------|-----|---|---------------------|
| 25 | 1755   | 36.7 | 930 | 3 | AAAY90240 Chlamydia |
| 26 | 1734   | 36.3 | 936 | 3 | AAAY9842 Chlamydia  |
| 27 | 1734   | 36.3 | 936 | 5 | ABB90602 Chlamydia  |
| 28 | 1734   | 36.3 | 936 | 6 | ABU26755 Protein e  |
| 29 | 1732   | 36.2 | 914 | 2 | AAW88429 Chlamydia  |
| 30 | 1705   | 35.7 | 925 | 3 | AAAY9843 Chlamydia  |
| 31 | 1685   | 35.2 | 885 | 3 | AAAY90238 Chlamydia |
| 32 | 1634.5 | 34.2 | 945 | 3 | AAAY9368 Mature Ch  |
| 33 | 1621.5 | 33.9 | 945 | 2 | AAW88428 Amino aci  |
| 34 | 1562.5 | 32.7 | 839 | 5 | ABP56002 Chlamydia  |
| 35 | 1562.5 | 32.7 | 839 | 5 | ABB98211 Chlamydia  |
| 36 | 1562.5 | 32.7 | 839 | 6 | ABU6287 C. psitt    |
| 37 | 1535   | 32.1 | 746 | 5 | ABB90535 Chlamydia  |
| 38 | 1435.5 | 30.0 | 841 | 5 | ABB90595 Chlamydia  |
| 39 | 1435.5 | 30.0 | 841 | 6 | ABU26753 Protein e  |
| 40 | 1432.5 | 30.0 | 841 | 2 | AAAY92818 Chlamydia |
| 41 | 1429.5 | 29.9 | 841 | 2 | AAW88420 Chlamydia  |
| 42 | 1353   | 28.3 | 922 | 5 | ABB90546 Chlamydia  |
| 43 | 1348   | 28.2 | 922 | 3 | AAAY95548 Chlamydia |
| 44 | 1345   | 28.1 | 922 | 2 | AAAY34597 Chlamydia |
| 45 | 1344   | 28.1 | 922 | 2 | AAW88419 Chlamydia  |

## ALIGNMENTS

RESULT 1  
AAW88417  
ID AAW88417 standard; protein; 928 AA.  
XX  
AC AAW88417;  
XX  
DT 17-OCT-2003 (revised)  
DT 26-APR-1999 (first entry)  
XX  
DE Chlamydia pneumoniae surface exposed protein Omp4.  
XX  
KW Omp4; outer membrane protein 4; surface exposed protein; antigen;  
infection; diagnosis; vaccine; atherosclerosis; asthma.  
XX  
OS Chlamydia pneumoniae.  
XX  
PN WO9858953-A2.  
XX  
PD 30-DEC-1998.  
XX  
PF 19-JUN-1998; 98WO-DK000266.  
XX  
PR 23-JUN-1997; 97DK-0000744.  
XX  
PA (BIRK/) BIRKELUND S.  
PA (CHR/) CHRISTIANSEN G.  
XX  
PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;  
WPI: 1999-105610/09.  
DR N-PSDB; AAX06816.  
XX  
PT Species-specific test for identifying mammals infected with Chlamydia  
pneumoniae - comprises detecting antibodies specific for outer membrane  
proteins of C. pneumoniae or nucleic acids encoding these proteins.  
XX  
PS Claim 7; Page 40-42; 115pp; English.  
XX  
CC This polypeptide comprises the novel 98.9 kDa surface exposed protein  
Omp4 of the human respiratory pathogen Chlamydia pneumoniae. Its amino  
acid sequence was deduced from DNA (see AAX06816) isolated from a C.  
pneumoniae expression library. The invention provides 12 novel surface  
exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid  
sequences encoding them (see AAX06816-27). A new species specific test is  
claimed that is used to identify mammals (including humans) infected with  
Chlamydia pneumoniae. The test comprises detecting antibodies specific  
for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer

CC membrane proteins, especially by PCR. The proteins are also used in the  
 CC diagnosis of *C. pneumoniae* infection in mammals. The nucleic acids and  
 CC proteins can also be used in the immunization of mammals, the nucleic  
 CC acids being particularly useful as DNA vaccines for effecting *in vivo*  
 CC expression of antigens. The vaccines may also prevent atherosclerosis and  
 CC bronchial asthma, which are possibly associated with *C. pneumoniae*.  
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 928 AA;

Query Match 100.0%; Score 4782; DB 2; Length 928;

Best Local Similarity 100.0%; Pred. No. 5.1e-307; Mismatches 0; Gaps 0;

Matches 928; Conservative 0; Indels 0; Gaps 0;

QY 1 MKTSIPWLVSSVAFSCGHSLOSLANEELLSPDSEFNGIDSGFTPTPKTSATTTYSLTGDFV 60  
 DB 1 MKTSIPWLVSSVAFSCGHSLOSLANEELLSPDSEFNGIDSGFTPTPKTSATTTYSLTGDFV 60  
 QY 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIADGTHAGAASTTANKNLTFSGFS 120  
 DB 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIADGTHAGAASTTANKNLTFSGFS 120  
 QY 121 LLSFDSSTPTVTGQGTLSAGGVNLENIRKLVVAGNFTADGAIKGAFLITGTSGD 180  
 DB 121 LLSFDSSTPTVTGQGTLSAGGVNLENIRKLVVAGNFTADGAIKGAFLITGTSGD 180  
 QY 181 ALFENNSSTKGAIATTAGARIANTGYVFLNINASTSGAIDDEGTSLSNKFLYF 240  
 DB 181 ALFENNSSTKGAIATTAGARIANTGYVFLNINASTSGAIDDEGTSLSNKFLYF 240  
 QY 241 EGNAAKTGGAI CNTKASGPELII SNKTLIPASNAETS GGAIIHAKKALSSGGFTFEP 300  
 DB 241 EGNAAKTGGAI CNTKASGPELII SNKTLIPASNAETS GGAIIHAKKALSSGGFTFEP 300  
 QY 301 LRRNVSSATPKGAIISIDAGELSDSAGTNTVTRNLTGTSSTPDKVAINIGSNGK 360  
 DB 301 LRRNVSSATPKGAIISIDAGELSDSAGTNTVTRNLTGTSSTPDKVAINIGSNGK 360  
 QY 361 FTELRAAKNHTIFPYDPTTSGTSSDVKINNGSAGALNPYQGITLFSGETLTDELKVA 420  
 DB 361 FTELRAAKNHTIFPYDPTTSGTSSDVKINNGSAGALNPYQGITLFSGETLTDELKVA 420  
 QY 421 DNLSKSFQPVSLSGSKLLQKGVTLBESTSFSEAGSLLGMDSGTTLSTAGSITITNLG 480  
 DB 421 DNLSKSFQPVSLSGSKLLQKGVTLBESTSFSEAGSLLGMDSGTTLSTAGSITITNLG 480  
 QY 481 INVDSLGIKQVSLTAKGASNKVIVSGKLNIDIEGNIYESHMSHDQLFSLKITYDAD 540  
 DB 481 INVDSLGIKQVSLTAKGASNKVIVSGKLNIDIEGNIYESHMSHDQLFSLKITYDAD 540  
 QY 541 VDTNVDISLLIPVPAEDPNSSEYFGQGNVMTTDTATNTKEATYATWTKTGFVSPERKS 600  
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 QY 661 VYIGSSATTPKDDLTFAFCHLFAADKCCFLAHNNSRYGGLTFKSHHTLOPQNYLRLG 720  
 DB 661 VYIGSSATTPKDDLTFAFCHLFAADKCCFLAHNNSRYGGLTFKSHHTLOPQNYLRLG 720  
 QY 721 RAKFESASIEKFPREIPLALDVQVFSHSDNRMETHTSLPESBSWNECIAGIGIDL 780  
 DB 721 RAKFESASIEKFPREIPLALDVQVFSHSDNRMETHTSLPESBSWNECIAGIGIDL 780  
 QY 781 PFLVSNPPLPFXTFILPQMKVEMVYVSSQNSFFESSSDGSGFSIGRLNLISIPVGAFFVGD 840  
 DB 781 PFLVSNPPLPFXTFILPQMKVEMVYVSSQNSFFESSSDGSGFSIGRLNLISIPVGAFFVGD 840  
 QY 841 IGDSTTYLDSGFVSDVYRNPNQSTATLYMSFDSWKIRGNSLRQAFLLRGSNNYVNSN 900  
 DB 841 IGDSTTYLDSGFVSDVYRNPNQSTATLYMSFDSWKIRGNSLRQAFLLRGSNNYVNSN 900

QY 901 CELFGHYAMELRGSSRNRYVDYGTKLRF 928  
 DB 901 CELFGHYAMELRGSSRNRYVDYGTKLRF 928

# RESULT 2

AA90236  
 ID AAY90236 standard; protein; 928 AA.

AC AAY90236;

DT 12-SEP-2003 (revised)  
 DT 29-AUG-2000 (first entry)

DE Chlamydia antigen CPN100634.

KM Chlamydia antigen; diagnosis; infection; community acquired pneumonia;  
 KW therapy; upper respiratory tract disease; bronchitis; sinusitis;  
 KW aethmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.

OS Chlamydia pneumoniae.

XX W0200032794-A2.

PD 08-JUN-2000.

PE 01-DEC-1999; 99MO-CA001147.

XX 01-DEC-1998; 98US-0110339P.

PR 01-DEC-1998; 98US-0110340P.

PR 01-DEC-1998; 98US-0110427P.

PR 01-DEC-1998; 98US-0110428P.

PR 01-DEC-1998; 98US-0110438P.

XX (CONN-) CONNAUGHT LAB LTD.

XX Murdin AD, Oomen RP, Wang J;

XX WPI: 2000-412339/35.

DR N-PSDB; AAA30847, AAA30848.

XX Nucleic acids encoding polypeptide antigens from Chlamydia useful for

PT preventing, diagnosing and treating diseases such as community acquired

PT pneumonia, bronchitis, sinusitis and aethmatic bronchitis, adult-onset

PT asthma.

XX Claim 16; Fig 1; 174pp; English.

CC This sequence is a Chlamydia antigen of the invention, designated  
 CC CPN100634. The nucleic acids (and their complementary sequences) may be  
 CC used as diagnostic agents for detecting the presence of nucleic acids  
 CC encoding Chlamydia antigens in samples according to standard methods, and  
 CC therefore, for diagnosing Chlamydia infections. For example, they may be  
 CC used as primers and probes for diagnostic polymerase chain reaction (PCR)  
 CC assays. Antisense sequences may be used to down regulate expression of  
 CC the proteins and may be used to treat infections. The nucleic acids may  
 CC also be used to produce the protein antigens they encode according to  
 CC standard recombinant DNA methodologies. The proteins may then be used as  
 CC antigens for the production of antibodies (i.e. as vaccines) for  
 CC preventing infection by Chlamydia. The antibodies may also be used as  
 CC diagnostic reagents for detecting infections. Chlamydia is a pathogen  
 CC implicated in the development of (for example) community acquired  
 CC pneumonia, upper respiratory tract disease (especially bronchitis and  
 CC sinusitis, aethmatic bronchitis, adult-onset asthma and acute  
 CC exacerbations of asthma in adults. (Updated on 12-SEP-2003 to standardise  
 CC OS field)

XX Sequence 928 AA;

Query Match 100.0%; Score 4782; DB 3; Length 928;

Best Local Similarity 100.0%; Pred. No. 5.1e-307; Mismatches 0; Gaps 0;

Matches 928; Conservative 0; Indels 0; Gaps 0;

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 DB 121 LLSFDDSPSTVTYTGQGLSSAGVNLNTRKLVNAGNFTAGGAIKGSFLLTGSGD 180  
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 DB 181 ALFSSNNSSSTKGALATTAGARIANNTRYRPLSNLSTSGAIDDEGTSILSNKFLYF 240  
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 DB 241 EGNAAKTGGALCNTYKASGSPPELLISNNKTLIPASNAETSGAIIHAKKLALSSGGFTEF 300  
 QY 301 LRRNVSATPKGALSTDAAGELSLAETGNITFVRNTLITTSSTDPKRNAINIGSNGK 360  
 DB 301 LRRNVSATPKGALSTDAAGELSLAETGNITFVRNTLITTSSTDPKRNAINIGSNGK 360  
 QY 361 FTFLRAAKNTTIFFYDPTTSEGTSDVLKINNSAGALNPFYQGTILFSGETTLTADLKVA 420  
 DB 361 FTFLRAAKNTTIFFYDPTTSEGTSDVLKINNSAGALNPFYQGTILFSGETTLTADLKVA 420  
 QY 421 DNKSSFTQPVSLSGCKLLQKGVLESTSPSOEAGSLQMDSGTLLSTTASITTTNIG 480  
 DB 421 DNKSSFTQPVSLSGCKLLQKGVLESTSPSOEAGSLQMDSGTLLSTTASITTTNIG 480  
 QY 481 INVDSLGLKQPVSLTAKGANKYIVSGKLLIDIEGIVSSHMFSDQLFSLKITVDAD 540  
 DB 481 INVDSLGLKQPVSLTAKGANKYIVSGKLLIDIEGIVSSHMFSDQLFSLKITVDAD 540  
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 DB 541 VDTNVDISLLIPPAEDPNSEYFGQGMVNTTDTATNTKEATATWTKTGFVPSPERKS 600  
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 DB 661 YVIGGSANHTPKDULFFAFCHLPARDKCFIAHNSNTTGGTLPFKKSHLQONYLRLG 720  
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 DB 901 CELFGHYAMELRGSSRRYVNDVGTKLRF 928

RESULT 3  
 ABB90583  
 ID ABB90583 standard; protein; 928 AA.  
 AC ABB90583;  
 XX  
 DT 29-AUG-2003 (revised)

DT 29-JUL-2002 (first entry)  
 XX Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.  
 DE Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.  
 XX Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.  
 KW Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.  
 KW human respiratory disease; cardiovascular disease; atherosclerosis;  
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;  
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;  
 KW strain CWL029.  
 XX Chlamydia pneumoniae.  
 OS Chlamydia pneumoniae.  
 XX Chlamydia pneumoniae.  
 FH Key Location/Qualifiers  
 FT Peptide 1..17  
 FT Protein /label= Signal\_peptide  
 FT Protein 18..928  
 FT Protein /note= "mature protein"  
 PN MO200202606-A2.  
 XX MO200202606-A2.  
 PD 10-JAN-2002.  
 XX 10-JAN-2002.  
 PD 03-JUL-2001; 2001WC-IB001445.  
 XX 03-JUL-2001; 2001WC-IB001445.  
 PR 03-JUL-2000; 2000GB-00016363.  
 PR 11-JUL-2000; 2000GB-00017047.  
 PR 21-JUL-2000; 2000GB-00017983.  
 PR 07-AUG-2000; 2000GB-00019368.  
 PR 18-AUG-2000; 2000GB-00020440.  
 PR 14-SEP-2000; 2000GB-00022583.  
 PR 10-NOV-2000; 2000GB-00027549.  
 PR 22-DEC-2000; 2000GB-00031706.  
 XX (CHIR-) CHIRON SPA.  
 XX Ratti G, Grandi G;  
 DT N-PSDB; ABL91241.  
 DR WPI; 2002-154726/20.  
 XX N-PSDB; ABL91241.  
 XX Novel Chlamydia pneumoniae protein useful in the manufacture of a  
 PT medicament for treatment or prevention of infection due to Chlamydia,  
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.  
 PS Claim 1; Page 96-97; 364pp; English.  
 XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia  
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding  
 CC them. The proteins are predicted to be immunogenic and may therefore be  
 CC useful in vaccine production and for diagnostic purposes. Chlamydia  
 CC pneumoniae is a common cause of respiratory disease in humans, and is  
 CC also involved in the development of cardiovascular diseases such as  
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,  
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,  
 CC claudication and stroke. The proteins and nucleic acids of the invention  
 CC may be used in vaccines and pharmaceutical compositions for the  
 CC prevention or treatment of chlamydial infections, particularly Chlamydia  
 CC pneumoniae infections. The proteins may also be used in the detection of  
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched  
 CC DNA probe assay or blotting techniques for determining Chlamydia  
 CC pneumoniae gene expression. The present sequence represents a  
 CC specifically claimed Chlamydia pneumoniae protein of the invention.  
 CC (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 928 AA;  
 Query Match 100.0%; Score 4782; DB 5; Length 928;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-307;  
 Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSLPWLVSVLAFSCHLQSLANEELSPDDSFNGNIDSGTTPPKTSATTYSLTGDFV 60  
 DB 1 MKTSLPWLVSVLAFSCHLQSLANEELSPDDSFNGNIDSGTTPPKTSATTYSLTGDFV 60

```

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DB 61 FVEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGLDAGTHAGAASTANKNLTFSGFS 120
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DB 121 LLSFDSSTPTVTTCGCTSSAGVNLNIRKLVVAGNESTADGAIKGAFLITGSGD 180
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DB 181 ALFSSNNSSSTKGGAIATTAAGARIANNNGYRPLSNLTASTGGAIIDEGSTIILSNKPLYF 240
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DB 301 LRNNVSATPKGGAISIDASGELSLSAETGNITFVRNTLTGSGTDPKKNALINISNGK 360
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DB 361 FTBLRAKNNHTTFYDPTSEBTSVDLKTINNSAGALNFPYQGITLPSGETLADDELKVA 420
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DB 421 DNLSKSFQPVSLSGKLLQKGVTLSESTFSQFAGSLLGWDSGTTLTAGSITITNLG 480
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DB 481 INVDSLGLKOPVSLTAKGASNKVIVSGKLNIDIEGNIYESHMSHDLQFLSKITVDAD 540
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DB 601 ALVNCNTMGVFTDIRSLQQLVEIGATGMEHKGFVWSMTNLFHKTDENRKGFRTSGG 660
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DB 721 RAKSESSEIEKPEPEIPLADVVSFSHSDNRMEHTHTSLPESGSMNECTIAGIGIDL 780
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DB 841 IGDSTYTDLSGFPVSDVYRNNPOSTATILVMSPDWKIRGKULSQAFLIRGSNNYVYNSN 900
QY 901 CELFGHYAMELRGSSRRNVNDVGTKLRF 928
DB 901 CELFGHYAMELRGSSRRNVNDVGTKLRF 928

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RESULT 4  
ABU26757 standard; protein, 928 AA.

ABU26757;  
23-OCT-2003 (revised)  
19-JUN-2003 (first entry)  
Protein encoded by Prokaryotic essential gene #12284.

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX Chlamydomonada pneumoniae.  
OS Chlamydomonada pneumoniae.  
XX Chlamydomonada pneumoniae.  
PN WO200277183-A2.  
XX 03-OCT-2002.  
XX 21-MAR-2002; 2002WO-US009107.  
XX 21-MAR-2001; 2001US-00815242.  
XX 06-SEP-2001; 2001US-00948993.  
XX 25-OCT-2001; 2001US-0342823P.  
XX 08-FEB-2002; 2002US-00072851.  
XX 06-MAR-2002; 2002US-0362699P.  
XX (ELIT-) ELITRA PHARM INC.  
PA Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlsen KU, Zykind JW, Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH, WPI: 2003-029926/02.  
DR N-PSDB; ACA30627.  
DR New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.  
PT Claim 25; SEQ ID NO 54681; 1766bp; English.  
PS The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 23-OCT-2003 to standardise OS field)

SO Sequence 928 AA;  
Query Match 100.0%; Score 4782; DB 6; Length 928;  
Best Local Similarity 100.0%; Pred. No. 5.1e-307; Indels 0; Gaps 0;  
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTISIPWLVSSVLAFCCHLOSLANEELSLPDDSFNGNINSGTFTPTKTSATYSLTGVDF 60  
DB 1 MKTISIPWLVSSVLAFCCHLOSLANEELSLPDDSFNGNINSGTFTPTKTSATYSLTGVDF 60



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QY 61 FYBPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFEGFIDAGTHAGAASTTANKULTFSGFS 120
DB 61 FYBPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFEGFIDAGTHAGAASTTANKULTFSGFS 120
QY 121 LLSFDSSTPTVTTGGTGLSSAGVNLLENIRKLVVAGNFTAGGAIKGAFLITGTSGD 180
DB 121 LLSFDSSTPTVTTGGTGLSSAGVNLLENIRKLVVAGNFTAGGAIKGAFLITGTSGD 180
QY 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
DB 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAKTTGGAICNTKASGSPPELLISNNKTLIFASVVAETSGAIIHAKKALASSGGFTTF 300
DB 241 EGNAAKTTGGAICNTKASGSPPELLISNNKTLIFASVVAETSGAIIHAKKALASSGGFTTF 300
QY 301 LRNNVSSATPKGGAISIDASGELSIAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 360
DB 301 LRNNVSSATPKGGAISIDASGELSIAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 360
QY 361 FTFLRAAKNHTIFFYDPTISEGTSVDLKIINSGAGALNPYOGTILFSGETTLADELKVA 420
DB 361 FTFLRAAKNHTIFFYDPTISEGTSVDLKIINSGAGALNPYOGTILFSGETTLADELKVA 420
QY 421 DNLKSSFTQPVSLSGKLLLOKGVLTLESTFSQEGASLLGMDSGTTLSTTAGSITITNLG 480
DB 421 DNLKSSFTQPVSLSGKLLLOKGVLTLESTFSQEGASLLGMDSGTTLSTTAGSITITNLG 480
QY 481 INVDISLGLKQPVSLTAKGASNKIVSGKLLIDIEGNIYSHMFSDHQLFKITYDAD 540
DB 481 INVDISLGLKQPVSLTAKGASNKIVSGKLLIDIEGNIYSHMFSDHQLFKITYDAD 540
QY 541 VDTNVDISLIPPAEDPNSEYGFQGGOMVNMWTTDTATNTKATATWTKGFPVSPERKS 600
DB 541 VDTNVDISLIPPAEDPNSEYGFQGGOMVNMWTTDTATNTKATATWTKGFPVSPERKS 600
QY 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVSSMTNPLHKTGDENRKGFRHTSGG 660
DB 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVSSMTNPLHKTGDENRKGFRHTSGG 660
QY 661 YVIGGSAHTPKDULFTFAFCHLFAKPDGCIANNSSTYGGTLPFKKSHTLQONTIARLG 720
DB 661 YVIGGSAHTPKDULFTFAFCHLFAKPDGCIANNSSTYGGTLPFKKSHTLQONTIARLG 720
QY 721 RAKFSSEAIKPREIPLALDVQVSFSHSDNRMEHTTSLPESGGSNNEICIAGGIGLGL 780
DB 721 RAKFSSEAIKPREIPLALDVQVSFSHSDNRMEHTTSLPESGGSNNEICIAGGIGLGL 780
QY 781 PVLASNPHLPFKTFIPQMKVEMYVVSQNSFFESSSDGRGFSIGRLNLSIPVAKKPYQGD 840
DB 781 PVLASNPHLPFKTFIPQMKVEMYVVSQNSFFESSSDGRGFSIGRLNLSIPVAKKPYQGD 840
QY 841 IGGSTYTDLSGFVSDVYRNNPOSTATLVMSPDWKIRGNLSROAFLRGSNNYYNSN 900
DB 841 IGGSTYTDLSGFVSDVYRNNPOSTATLVMSPDWKIRGNLSROAFLRGSNNYYNSN 900
QY 901 CELFGHYAMELRGSSRRYNDVGTCLRF 928
DB 901 CELFGHYAMELRGSSRRYNDVGTCLRF 928

RESULT 5
AAV35060
ID AAV35060 standard; protein; 949 AA.
XX
AC AAV35060;
XX
XX 17-OCT-2003 (revised)
DT 13-SEP-1999 (first entry)
XX
DE Chlamydia pneumoniae cellular envelope protein.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
```

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KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope.
OS Chlamydia pneumoniae.
PN MO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98MO-1B001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST ) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT
PS Genome sequence of Chlamydia pneumoniae.
XX
PS Page 947-949; Disclosure; 1912pp; English.
XX
CC AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAY91990) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 949 AA;

Query Match 99.8%; Score 4774; DB 2; Length 949;
Best Local Similarity 99.9%; Pred. No. 1.8e-306;
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTSLPVLVSVSLAFSCHLQSLANBELLPDPSFNGNIDSGFTPKTSATYSLTGDF 60
DB 22 MKTSLPVLVSVSLAFSCHLQSLANBELLPDPSFNGNIDSGFTPKTSATYSLTGDF 81
QY 61 FYBPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFEGFIDAGTHAGAASTTANKULTFSGFS 120
DB 82 FYBPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFEGFIDAGTHAGAASTTANKULTFSGFS 141
QY 121 LLSFDSSTPTVTTGGTGLSSAGVNLLENIRKLVVAGNFTAGGAIKGAFLITGTSGD 180
DB 142 LLSFDSSTPTVTTGGTGLSSAGVNLLENIRKLVVAGNFTAGGAIKGAFLITGTSGD 201
QY 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
DB 202 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 261
QY 241 EGNAAKTTGGAICNTKASGSPPELLISNNKTLIFASVVAETSGAIIHAKKALASSGGFTTF 300
DB 262 EGNAAKTTGGAICNTKASGSPPELLISNNKTLIFASVVAETSGAIIHAKKALASSGGFTTF 321
QY 301 LRNNVSSATPKGGAISIDASGELSIAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 360
DB 322 LRNNVSSATPKGGAISIDASGELSIAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 381
QY 361 FTFLRAAKNHTIFFYDPTISEGTSVDLKIINSGAGALNPYOGTILFSGETTLADELKVA 420
DB 382 FTFLRAAKNHTIFFYDPTISEGTSVDLKIINSGAGALNPYOGTILFSGETTLADELKVA 441
QY 421 DNLKSSFTQPVSLSGKLLLOKGVLTLESTFSQEGASLLGMDSGTTLSTTAGSITITNLG 480
DB 442 DNLKSSFTQPVSLSGKLLLOKGVLTLESTFSQEGASLLGMDSGTTLSTTAGSITITNLG 501
```

QY 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITVDAD 540  
XX |||||  
Db 502 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITVDAD 561  
QY 541 VDTNVDISLIPVPAEDPNSSEYFGQGMNVMTTDTATNTKEATATWTGTGFVSPERKS 600  
XX |||||  
Db 562 VDTNVDISLIPVPAEDPNSSEYFGQGMNVMTTDTATNTKEATATWTGTGFVSPERKS 621  
QY 601 ALVNTLMAGVFTDIRSLQQLVEIGATGMEHKQGFVWSMTNPLHKTGDENRKGFRHTSGG 660  
XX |||||  
Db 622 ALVNTLMAGVFTDIRSLQQLVEIGATGMEHKQGFVWSMTNPLHKTGDENRKGFRHTSGG 681  
QY 661 YVIGSAHTPKDGLFTFAFCHLFAKDQCFIAHNNNSRTYGGTLFFKSHHTLQPNYLRIG 720  
XX |||||  
Db 682 YVIGSAHTPKDGLFTFAFCHLFAKDQCFIAHNNNSRTYGGTLFFKSHHTLQPNYLRIG 741  
QY 721 RAKFSESAIEKFPREIPLALDVQVSFSHSDNRMTHTYSLPESGGSNNECIAAGIGLDL 780  
XX |||||  
Db 742 RAKFSESAIEKFPREIPLALDVQVSFSHSDNRMTHTYSLPESGGSNNECIAAGIGLDL 801  
QY 781 PFVLSNPHPLFKFTIPQMKVEMVYVVSQNSPFSSSDGSGFISGLNLMSIPVGAKEVQGD 840  
XX |||||  
Db 802 PFVLSNPHPLFKFTIPQMKVEMVYVVSQNSPFSSSDGSGFISGLNLMSIPVGAKEVQGD 861  
QY 841 IGDSTYDLSGFPVSDVYRNNDPOSTATLVMSPDMSKIRGNI.SRQAFLLRGSNNYVYNSN 900  
XX |||||  
Db 862 IGDSTYDLSGFPVSDVYRNNDPOSTATLVMSPDMSKIRGNI.SRQAFLLRGSNNYVYNSN 921  
QY 901 CELFGHYAMELRGSSRNNTVDVGTKLRF 928  
XX |||||  
Db 922 CELFGHYAMELRGSSRNNTVDVGTKLRF 949

## RESULT 6

AA69369

ID AA69369 standard; protein; 918 AA.

AA69369;

AC

AA69369;

XX

DT 12-SEP-2003 (revised)

DT 19-JUN-2000 (first entry)

XX

DE Amino acid sequence of the CPN100395 polypeptide.

XX

KM CPN100395; Chlamydia infection; immune response; vaccine.

XX

OS Chlamydia pneumoniae.

XX

PN WO200011183-A2.

PD

02-MAR-2000.

XX

18-AUG-1999; 99WO-IB001449.

XX

20-AUG-1998; 98US-0097187P.

XX

20-AUG-1998; 98US-0097188P.

XX

20-AUG-1998; 98US-0097189P.

XX

20-AUG-1998; 98US-0097190P.

XX

20-AUG-1998; 98US-0097195P.

XX

20-AUG-1998; 98US-0097196P.

XX

20-AUG-1998; 98US-0097197P.

XX

27-AUG-1998; 98US-0097191P.

XX

17-AUG-1999; 99US-00376770.

XX

(CONN-) CONNNAUGHT LAB LTD.

XX

Murdin AD, Oomen RP;

XX

WPI: 2000-224703/19.

XX

N-PSDB; AAZ61509.

XX

Novel antigens and corresponding DNA molecules that can be used to

PT prevent, treat and diagnose disease caused by Chlamydia infection in  
PT mammals, especially humans.

PS Claim 19; Fig 15-E; 201pp; English.

XX AA69362-69 represent Chlamydia pneumoniae polypeptides. The polypeptides  
CC are present in the bacterial membrane structure, in the external vicinity  
CC of the membrane structure, in the inclusion membrane structure, in the  
CC external vicinity of the inclusion membrane structure, and in the  
CC cytoplasm of the infected cell. The polypeptides may be used to prevent,  
CC treat and detect the presence of Chlamydia infection and/or the presence  
CC of Chlamydia in a sample. The vaccine vector comprising the  
CC immune response in a mammal. The vaccine vector comprising the  
CC polynucleotides is used to induce an immune response in a mammal.  
CC Antibodies directed against the polypeptides may also be used  
CC therapeutically to treat and/or prevent a Chlamydia infection. (Updated  
CC on 12-SEP-2003 to standardise OS field)

XX Sequence 918 AA;

SQ Query Match 38.9%; Score 1862; DB 3; Length 918;

Best Local Similarity 42.3%; Pred. No. 4, 9e-114; Mismatches 352; Indels 34; Gaps 12;

Matches 398; Conservative 156; Mismatches 352; Indels 34; Gaps 12;

QY 1 MKTSPWLVSVLAFSCHIQL-ANBELSPDPSFGNIDSGFTTPK-----TSATT 52  
XX |||||  
Db 1 MRSSPSLILISSLAEPPL-LMSVSADAADLTLSRDSYNDGTSSTFEPRKATSDAGTT 59  
XX |||||  
QY 53 YSLTGVFFPEPKGPIPLDSCEKOTPDNLTFIGNHSLTFPGTIDGTNAGAASTTANK 112  
XX |||||  
Db 60 YILDGVVISQAGKQTSLTSSCSNTAGNLTFGNGFSLFDNIISTVAGVVSITPAS 119  
XX |||||  
QY 113 NLT-FSGFSLSPDSSPTVTVTGOGTLSAGGVNLENIKLVAAGNFTADGAIKAS 171  
XX |||||  
Db 120 GITKFSGFTLMLAAR--TTGKAIKITDGLVESIGNLNLNENASENGALINTKT 176  
XX |||||  
QY 172 FLITGTSGLALFSSNSSSTYTGAIATTAGKRIANNTRYFLSNISTSGALIDDEGT 231  
XX |||||  
Db 177 LSLTGSTRFVAFPLGNSSQCGAIYASGDSVISENAGILSFGNNSATTSOGAISAGCNV 236  
XX |||||  
QY 232 LSNKKFLYFEGNAKTTGAIICNTKASGSP--LISNNKTLFASVATSGAIIHAK 289  
XX |||||  
Db 237 ISNNQNIFFDGCATTNGAIDCNKAGANDPDLTILSGNSLHFLNNTAENSAGALYTK 296  
XX |||||  
QY 290 LALSQG-GTFEFLRNWVSATPKGAISIDAGELSLAETGNIITFVRNTLTGSTDTP 348  
XX |||||  
Db 297 LVLSGKGVLFNNKKAANTPKGAIALIDSGEISISADLGNITFEGNTTSTGSPASV 356  
XX |||||  
QY 349 KRNAINIGSNGKTELRPAKNTIIFYPDPTSGTSSDVLTINNAGALNPIQGTILFS 408  
XX |||||  
Db 357 TRNAIDLASNAKFLNLRATGNKVIFYPDPTSSG-ATDKLSLNKADAGSGNTVEGYIVFS 415  
XX |||||  
QY 409 GETTDELKVAADLVKSSFTQPVSLSGGKLLKQGVTLSTSPQASGLLGDGSTTLS 468  
XX |||||  
Db 416 GKKLSBELKKPDVLASTFTQAVELAGALVLKQGVTVANTTTQVEGSKVYMDGGTTFE 475  
XX |||||  
QY 469 TTGASITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQ 528  
XX |||||  
Db 476 ASAGVTLNGLAINISLDGNTKAIKATTAASDVALSGLIMLVDAQNYEHNHLSQQQ 535  
XX |||||  
QY 529 LFSLLKTTVDADVDTNVDISLIPVPAEDPNSSEYFGQGMNVMTTDTATNTKEATATWT 588  
XX |||||  
Db 536 VFPLIEISAOGTW-TTVDIPD---TPIANTNNHYGQGMNIVWVDATKATKNAALTLWT 591  
XX |||||  
QY 589 KTGFPVSPERKSLVQNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVWSMTNPLHKTGD 648  
XX |||||  
Db 592 KTGKPNPERQGPLVWSLWGSFVDSIQSLMDRSTSSLSSTNPLVSGIADFLYHEDQ 651  
XX |||||  
QY 649 ENRKGFRHTSGGYVIGSAHTPKDGLFTFAFCHLFAKDQCFIAHNNNSRTYGGTLFFKHS 708  
XX |||||  
Db 652 GNGRSYHSSAGYALGGFFTTASBNFNFACQLFGYDXDHVLAKNHTHYAAGMSYRH- 710  
XX |||||  
QY 709 HTLOPQNYLRIGRAKFSESAIEKFPREIPLALDVQVSFSHSDNRMTHTYSLPESGGS 768  
XX |||||

Db 711 -----LGSKTLAKLILSGNSDLPFVFNARFAYGHTDNNMTTKYGYSPVVGSMG 760  
Qy 769 NECIAGSIGLDLPVLSNPHPLKFTPIPOKKEVMVYVYSONSPRESSDGRGSGICRLNLT 828  
Db 761 NDAFGEICGGAIVVYVSGRRSWDTHTPTPLNLENTIAHQNDKENGEGSGSPGSEDLFNL 820  
Qy 829 SIPVGAKEVGDIGDSTYTDLSGFPVSDVYRNNPOSTATLWMSPDGKIRGNLSRQAF 888  
Db 821 AVPVGKIFEK--PDSKSTYDLSIAYVPDVIKNDPGCTTLLWSDGDSWSTGTSLSRQALL 878  
Qy 889 LRGSNNVYVNSCELFGHYAMELRGSSRRYNNVDVGTKLRF 928  
Db 879 VRAGNHAFASNFVEFQFEVELRGSSRSYALIDGGRFGF 918  
RESULT 7  
AAI94327  
ID AAY94327 standard; protein; 928 AA.  
AC AAY94327;  
XX  
XX  
DT 12-SEP-2003 (revised)  
DT 11-AUG-2000 (first entry)  
XX  
DE Chlamydia pneumoniae 98kD putative outer membrane protein.  
XX  
KM Chlamydia; antigen; vaccine; infection; outer membrane protein.  
XX  
OS Chlamydia pneumoniae.  
PN MO200026237-A2.  
PD 11-MAY-2000.  
XX  
PF 29-OCT-1999; 99MO-GH003579.  
XX  
PR 29-OCT-1998; 98US-0106070P.  
PR 01-MAR-1999; 99US-0122066P.  
PR 27-OCT-1999; 99US-00428122.  
XX  
PA (CONN-) CONNAUGHT LAB LTD.  
XX  
PI Murdin AD, Oomen RP, Dunn PL;  
XX  
XX WPI; 2000-365569/31.  
DR N-PSDB; AAA27021.  
XX  
PT Novel Chlamydia 98 kDa putative outer membrane protein antigen, used for  
XX vaccination and protection against Chlamydia infection.  
PS Claim 6; Fig 1; 93pp; English.  
XX  
XX The present sequence is the 98kDa putative outer membrane protein from  
CC Chlamydia pneumoniae. The genomic sequence was amplified using two PCR  
CC primers. The 5' primer contains a NotI restriction site, a ribosome  
CC binding site, an initiation codon and a sequence close to the 5' end of  
CC the 98kDa putative outer membrane protein coding sequence. The 3' primer  
CC contains the sequence encoding the C-terminal sequence of the putative  
CC outer membrane protein and a BspGI restriction site. The stop codon was  
CC excluded and an additional nucleotide was inserted to obtain an in-frame  
CC C-terminal fusion with the Histidine tag. The PCR product was cloned into  
CC a eukaryotic expression vector (pCA-Myc-His) by restricting both the  
CC vector and the PCR product with NotI and BamHI and performing a ligation  
CC reaction. This expression vector was injected intramuscularly and  
CC intranasally into mice, which were subsequently inoculated with Chlamydia  
CC pneumoniae. The chlamydial lung titers of the immunised mice were lower  
CC than those of the controls. Thus the 98kDa putative outer membrane  
CC protein can be used as a vaccine to provide protection against Chlamydia  
CC infections, especially Chlamydia pneumoniae infections. The present  
CC polypeptide may also be administered orally to treat Chlamydia infection.  
CC (Updated on 12-SEP-2003 to standardise OS field)  
XX

SQ Sequence 928 AA;  
Query Match 38.8%; Score 1855; DB 3; Length 928;  
Best Local Similarity 42.7%; Pred. No. 1,4e-113;  
Matches 405; Conservative 111; Mismatches 331; Indels 42; Gaps 20;  
Qy 1 MKTSLPVLVSSVLAFSCHLQSLANEELLSPDSEFNGNIDSGTFPPKTS----ATTYSLT 56  
Db 1 MKSSFPKFFVSTPAIFP--LSMIATETVLDSSASFPDGN-KGNPFVSRESQEDAGTYLPRK 57  
Qy 57 GVPFYE--RGKTPSLDSCFQKOTDNLTELGNGHSLTFPFIDAGTAGAAA--STTKNKL 114  
Db 58 GAVTLLENIPGTGATLYKSCFNNTKGDLPFTGNGNSLTFQTVAGVAGAAVNSVVDKST 117  
Qy 115 TFGSFLSLFSDSPSTVTYTGQTLIS-SAGVNLLENIRCLVAVNGFSTADGAIKASFL 173  
Db 118 TRIGPSLSFLIASPGSITTTGKAVSCSGSLSTKNVSLLSKSPSTNGAIIKTITS 177  
Qy 174 LTGTSGDALFSNNSSTKGAIAATTAGARIANNVGYRFLSNIASTSGAIDDEGTSILS 233  
Db 178 LGTTWSALFSENTSKKCGALQTSDALTYTNGQGVSPSDNTSSDGAIFTEASVTIS 237  
Qy 234 NKKFLYF-----EGNAAKTT---GCATNTAASGPBELIISNNKTLIFASNVAETSGA 284  
Db 238 NNAKVSFIDNKVTGASSTTGDMSGAICAYTSTDTKTLVGNQMLFSNNTSTTAGA 297  
Qy 285 IIAKKLASGSGFTEFLRNNVSAT--PKGASIDASGELSASRTGNTTFVRNTLTG 343  
Db 298 IYKKLELASGGTLTFSRNVNGGTAIPKGAIAIEGSLSSABSDGLVFLGNTVTSR 356  
Qy 344 STDTPKRNAININGKFTELRAKNHTIFFYDPIT--SEGTSDDVLKINSGALNPF 401  
Db 357 -TPGTNRSSIDIGTSKMTALRSAGRAIFYDPITGTSSTVTVDLKVNERPADALQY 415  
Qy 402 QGTILFSGEYLADELKAVDNKKSFTQPVSLSGKLLLOKVTLESTFSQDAGLLDM 461  
Db 416 TGNILFTGKLEBETAOSKNLTSKLOPVTLISGGLSLKMGVTLQTOAFTQOASRLDM 475  
Qy 462 DSGTTLSTAGSIITTNLGINVDSLGLKQPVSLTKAGSNKYIVSGKLNLIIEGNIYES 521  
Db 476 DVGTTLE-PADSTINNLVINISSIDGAKKAIETKATSKNLTLSGTTILLDPTGYFEN 534  
Qy 522 HMFSDQLFLKITYADVADVTNVDISSLIPVPAEDPNSERYGQGMN-VNMTTDTAINT 580  
Db 535 HSLRNPQSYDILELKASGTVTS---TAVTPDPIMGKPHYGYQGMGPBIVMGTAGSTT- 589  
Qy 581 KEATATWTTGTGVSPBKRSAIVCNTLKWGFVDISLQQLVEIGATGMHKQGFVWSMT 640  
Db 590 --ATFWWTGTGYIPNBERIGSLVPNSLWNAFIDISLHYMETANEGLOGDRAFWCAGS 647  
Qy 641 NFLAKTGDENRKGFPHTSQGVYIGSAHPKXDLFPFAPCHLPARDKCFIAHNNRTG 700  
Db 648 NFFHKDSTKTRRGFRLSGGYVIGNLHTCSPKSIASACQLFGRDRDFVAKNOGTVYG 707  
Qy 701 GTLFFGHSHTLPOPNYLRLGRAKFSBSALEKPRRIPALDVQVFSHSDNMEHTYSL 760  
Db 708 GTLYVQHNT-----YISL-PCKLRPCSLSYPTLIPVLSGNLSYTHDNDLKTYYTY 761  
Qy 761 PSESGWSNECTIAGGIGLDLPVLSNPHPLKFTPIPOKKEVMVYVYSONSPRESSDGRGF 820  
Db 762 PLYVKGWGDNSFALFEGGAPICL-DESALEFQYPMFMQLQFYVAHQBEFKGCEQAFARBF 820  
Qy 821 STGRLLNISIPVGAKE--VQGDIGDSTYTDLSGFPVSDVYRNNPOSTATLWMSPDGSKING 879  
Db 821 GSSRLVNLALPLGIRNDKESDCQDA-TYNLTLGYVVDLKRSPDCTTTLRIGSDSKWTFG 879  
Qy 880 GNLSRQAFLLRGSNNVYVNSCELFGHYAMELRGSSRRYNNVDVGTKLRF 928  
Db 880 TYLARGALVLRAGNHCFPCNSNFARFSQFSELRGSSRRYNNVDLGAKYQF 928  
RESULT 8  
AAW88421

|                       |    |   |
|-----------------------|----|---|
| ID                    |    | AAM88421 standard; protein; 928 AA.   |
| AC                    | XX |   |
| CC                    | XX | AAM88421;   |
| CT                    | XX | 17-OCT-2003 (revised)   |
| DT                    | XX | 26-APR-1999 (first entry)   |
| DE                    | XX | Chlamydia pneumoniae surface exposed protein Omp8.  |
| KV                    | XX | Omp8; Outer membrane protein 8; surface exposed protein; antigen;<br>infection; diagnosis; vaccine; atherosclerosis; asthma.  |
| OS                    | XX | Chlamydophila pneumoniae.   |
| PN                    | XX | W09858953-A2.   |
| PD                    | XX | 30-DEC-1998.  |
| PX                    | XX | 19-JUN-1998; 98WO-DK000266.   |
| PR                    | XX | 23-JUN-1997; 97DK-00000744.   |
| PA                    | XX | (BIRK/) BIRKELUND S.<br>(CHRI/) CHRISTIANSEN G.   |
| PI                    | XX | Birkelund S, Christiansen G, Knudsen K, Madsen A, Wgind P;<br>MPI; 1999-105610/09.  |
| DR                    | XX | N-PsDB; AAX06820.   |
| PT                    | XX | Species-specific test for identifying mammals infected with Chlamydia<br>pneumoniae - comprises detecting antibodies specific for outer membrane<br>proteins of C. pneumoniae or nucleic acids encoding these proteins.   |
| PS                    | XX | Claim 7; page 53-55; 115pp; English.  |
| CC                    | XX | This polypeptide comprises the novel 90.0 kDa surface exposed protein<br>Omp8 of the human respiratory pathogen Chlamydia pneumoniae. Its amino<br>acid sequence was deduced from DNA (see AAX06820) isolated from a C.<br>pneumoniae expression library. The invention provides 12 novel surface<br>exposed proteins, Omp4-Omp15 (see AAM88417-28), and nucleic acid<br>sequences encoding them (see AAX06816-27). A new species specific test is<br>claimed that is used to identify mammals (including humans) infected with<br>Chlamydia pneumoniae. The test comprises detecting antibodies specific<br>for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer<br>C membrane proteins, especially by PCR. The proteins are also used in the<br>diagnosis of C. pneumoniae infection in mammals. The nucleic acids and<br>proteins can also be used in the immunization of mammals, the nucleic<br>acids being particularly useful as DNA vaccines for effecting in vivo<br>expression of antigens. The vaccines may also prevent atherosclerosis and<br>bronchial asthma, which are possibly associated with C. pneumoniae.<br>(Updated on 17-Oct-2003 to standardise OS field) |
| SQ                    | XX | Sequence 928 AA:  |
| Query Match           |    | 38.7%; Score 1853; DB 2; Length 928;  |
| Best Local Similarity |    | 42.6%; Pred. No. 2e-113;  |
| Matches 404;          |    | Conservative 171; Mismatches 332; Indels 42; Gaps 20,   |
| QY                    |    | 1 MKTSTPWVLAVSVLAFSCHLOSLANBELISPPDSFNGNIDSGTFPPKTS---ATTYSILT 56   |
| Db                    |    | 1 MKSSFPKFVFSTFAIP--LSMIATETTVLDSSASFDGN-KKNQNFVRSEODAGTYLFK 57   |
| QY                    |    | 57 GVGFPE-GGKGPLSDSCFKOTDNLFLNGHSLTFPGFIAGHAGAA-STANKUL 114   |
| Db                    |    | 58 GNVTLENIIGTGTAIRKSCFNNTKGDLPFTGGNSLLFTVDAGIVGAADVSSVVDSKT 117  |
| QY                    |    | 115 TRSFGSLSFSDSPSTTTVGOGTLIS-SAGGVNLIENTRLVAANGFSTAAGAIKASFL 173   |
| Db                    |    | 118 TTFIIGESLFFIASRGSIITTKCAVCSTGSLKFDQNVSLFRSKPFSTDNGAIIAKTLIS 177   |
| QY                    |    | 174 LTGTSGDALFSNNSSSTKCGAIIATTAGARIANNTRYVRFSLNSTGSALIDDEGTSLIS 233   |

|           |   |   |     |   |
|-----------|---|---|-----|---|
| Db        | 178   | LGITWMSALFSENTSSKKGGAIQTSDBALTTIGNQGEVSPGDNTSSDGAALFTEASVTIS  | 23  | 7 |
| Qy        | 234   | NKFKELYF-----EGNAAKTT-----GCAICTKAGSGPELLISNNKTLIPASNAFESGCA  | 284 |   |
| Db        | 238   | NNAKVSPFNKTKTGASSSTTGDMGGACAAKTTSTDKVLTQOMLEFNNKSTTAGGA       | 297 |   |
| Qy        | 285   | IHKKTLALSSGGFTLELRNNVSAT-PKGAISISDAGSELSAETGNIIFVNVTLTTTG     | 343 |   |
| Db        | 298   | IYVKKLELSSGGTLTFSRNSVNGTAPKGAIIAIEDGSELSADSDIYFLNTYTSF        | 356 |   |
| Qy        | 344   | STDTPKRNAINIGSNGKFTELPAAKNHTIFFYDPT--SEGTSSDVAKINNSAGALNP     | 401 |   |
| Db        | 357   | -TGTNRSSIDIGTSAKMTALRSAGRAIIFYDDITGGSTTVVDLVKNEFTPADSALOY     | 415 |   |
| Qy        | 402   | QGITLPSGETLTADELKADNPKSSFTPPVSLSGSKLLLOKGYLTJESTSSQEAISLGM    | 461 |   |
| Db        | 416   | TGNIIFPTGKLTSETPAEDSKNLTSLDPPVTLSGGTLSLKKGVTLLQAFYQAADSLHEM   | 475 |   |
| Qy        | 462   | DSGTTLTSTAGSLTTNTNGINVDISGLQOPVSLAKAGASNKVVISGKLTNIDIEGNIYES  | 521 |   |
| Db        | 476   | DVGETLLE-PRDVTSTNNLVINISISIDGAKKAKIETKATSKNLTISGTTLLDPTGYEN   | 534 |   |
| Qy        | 522   | HMSHSHQLFSLKLTVDADVDTNVDISSLIPVPAEDPNSEYFGQGMN-VNMTTDTATNT    | 580 |   |
| Db        | 535   | HSLRNPQSDVILEKASGTVTS---FAVTBDPIKGEKFNHYGYGTGMPYWGTAATF-      | 589 |   |
| Qy        | 581   | KEATATWTKTGPVSPERKSALVCTLMGVTDIRLSLQQLVEIGATGMEHKQGFVWSMT     | 640 |   |
| Db        | 590   | --ATFPMWTKGYIPNBERIGSLVPSNINNAFIDISLHYMETANEGIQDGRAFWCAGLS    | 647 |   |
| Qy        | 641   | NFLHKTGDNKRGFRTSGGYVIGGSAHTPKDDIFTAFCHLFARDDCFIAHNNSRTYG      | 700 |   |
| Db        | 648   | NPFHKOSTYTRKGFRLSGGYVIGGNLHCTSDKILSAAFCQLFGRDDYFVAAKQGTIVG    | 707 |   |
| Qy        | 701   | GTEFFKXSHTLQFONTLRLGRAKFESESAIEKFPREIPLADVQVSPSHSDRMETHYSL    | 760 |   |
| Db        | 708   | GTLIYQHNEF-----YISL-PCKLRPCSLSYPTETIPLFSGNLSYHTDMDLTKYTTY     | 761 |   |
| Qy        | 761   | PESEGSNSNECIAAGIGLDLPFVLSPHPLEFKTFIPQMKVEMTVYVSONSPFESSSDGRGF | 820 |   |
| Db        | 762   | PLVAGSGWGNDSFALIEFGRAPICL-DESALFEQYMPFWKLOFVVAHOGFKEQCTEARF   | 820 |   |
| Qy        | 821   | SIGRLNLSIPVQAKF-VQGDIGDSYTYDLSGFFPSDYYRNNPOSTATVMSPDMSKIRG    | 879 |   |
| Db        | 821   | GSSGLVNLALPIGIRFDKESDCQDA-TYNLTLGYVDLVRSNPDCITTLRLISGDSMKTFG  | 879 |   |
| Qy        | 880   | GNLSRQAFILRGSNNVYNSNCELFEGHYAMELRGSSRYNAYDVGTKLRF             | 928 |   |
| Db        | 880   | TNLARQALVLRAGNHCFRNSFEALSQSFELRGSSRYNAYVDLAKYQF               | 928 |   |
| RESULT 9  |   |   |     |   |
| AAW884422 |   |   |     |   |
| ID        | AAW884422   | standard; protein; 918 AA.                                    |     |   |
| AC        | AAW884422;  |   |     |   |
| XX        |   |   |     |   |
| XX        | 17-OCT-2003 (revised)   |   |     |   |
| DT        | 26-APR-1999 (first entry)   |   |     |   |
| DE        | Chlamydia pneumoniae surface exposed protein Omp9.                |   |     |   |
| XX        |   |   |     |   |
| XX        | Omp9; outer membrane protein 9; surface exposed protein; antigen; |   |     |   |
| KW        | infection; diagnosis; vaccine; atherosclerosis; asthma.           |   |     |   |
| XX        |   |   |     |   |
| OS        | Chlamydia pneumoniae.   |   |     |   |
| PN        | W03658953-A2.   |   |     |   |
| XX        |   |   |     |   |
| PD        | 30-DEC-1998.  |   |     |   |
| PF        | 19-JUN-1998; 98KO-DK000266.                                       |   |     |   |
| XX        |   |   |     |   |



CC a C. psittaci antigen from the present invention. (Updated on 29-AUG-2003  
 CC to standardise OS field)  
 XX  
 SO Sequence 926 AA;

Query Match 37.7%; Score 1802; DB 5; Length 926;

Best Local Similarity 40.8%; Pred. No. 4,6e-110;  
 Matches 385; Conservative 172; Mismatches 354; Indels 32; Gaps 15;

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QY 1 MKTSIPWLVSSVLA--FSCHLQSLANBELSPDPSFNGNIDSGTFTPKTSAT--YS 54
D 1 MRBPLYKILISSTLTPLISFHSQLEHVALTGESIIDAN---GAFSPQSTSTAGGTIYN 57
QY 55 LTGDFVFEYEPGKPTLSDSCFKQTTDNLTFLNGHSLTFEFDAGTAGAAAATTANKL 114
D 58 VESDISIVDVQGTAAALASSAFVQJADNLTFRGNHSLISTANAGANPAGINVTADKIL 117
QY 115 TFSGFSLSFDPSSSTVTYTGQGTLSAGVNLNIRKLVVAGNFTADGAIKGSFLL 174
D 118 TLTFPSKLSFKECPSSLVNTGKAMKSGGALNANNSILFDQVYSAENGALISCKAFSL 177
QY 175 TGTSGDALFSNNSSTKGAIAATTAGARIANNQGVYFPLSIASTGAIIDEGTSLSN 234
D 178 TGSSKEISFTTNSSTAKKGAIAATGIAHLSDNQGTIFSGNTAVNSGAVYSEASMTIAG 237
QY 235 NKFLYFEGNAAKTT---GGAICNTKASGSPDLIISNNKTLIPASNAVETSGAIIHAKL 290
D 238 NNHVAFSNNAVSGSDCGGAHCSKTSAGPTLIRDKKVLIFPEINTSAAKGAIIYDKL 297
QY 291 ALSGCGFEPLRNWSSATPKGAI SIDAGELSIAETGNTTVRNTLTGSTDTPKR 350
D 298 ILTSGGPAFPINNKYATPKGAI GIAANEGCSLLEHGDITP-DNNLMTQDNATIKR 356
QY 351 NAININGSGKTELEAAKNHTIFFYDPTSECTSDVLKINNGSAGALNPGOTILFSGE 410
D 357 NAINIEGNGKVVNLRAASGKTIISFYDPTTVGNAADLTILKAGCD--KTYNGAILIFSGE 414
QY 411 TLTADELKVDNLKSSFTQPVLSGSKLLLOKGYLTLESTFSQEASILLGMDSGTTLSTT 470
D 415 KLTEBQAAVADNLKTTFTQPTTLAAGELVLSGVEVEKATVQVAGSILLMDAGTKLSAK 474
QY 471 AGSITTTMGINVDSLGKQVSLTAKASNKVIVSGKLNIDEGNIYESHMSHOLP 530
D 475 TEDATLTMLAINPMTLDGKRAVDAVAAGKVTLSGAI GVIDPTGKEYEHKLNIDLAL 534
QY 531 SLKLTVDADVDTNVDISLIPVPAEDPNSXFOGQNNWMTDTATNTEKATA--TWT 588
D 535 CGIQLSGKGSV--TTTNVPSHVGVAAE---THYGVGNMSVSWVDNNSDPKOTIAPFTWN 590
QY 589 KTGVPVSPERKSALVCNTLWGVFTDIRSLQOLVEIGATG-MEHKQGFVWSMTNPLAKTG 647
D 591 KTGVPVNERAPAPLVNLMSGFIDLRSLQVLEKSVDSILETRGLWVSGIGNFHDKR 650
QY 648 D-ENRKGRRHNSGCVITIGSANTPKDULPTAFCHLPARDQCFIAHNNSKTYGTLFEK 706
D 651 NAEENK-PRHISGCVGATNTTSREDSLSVAFCOLFAKDKQVYLSKNAANVYAGSVYYQ 709
QY 707 HSHLTQPNVYRLGAKFSESALIEKPREIPLALOVQFSFSDRMETHYSLPESGSG 766
D 710 HVSXKDDLTRLFNG---PNTCCSFSKEIPIFLDAQTTCYHTANMTTSTTDYEVGSG 765
QY 767 WSNECIAGIGLDPF-VLSNPHPLFKTFIPQMKVEMYVVSQNSFSESSDGRGFSIGRL 825
D 766 WONDTLGLTLSTVSPIPVFSS--SIFDSYAPPAKLVVYVAHQDDKEPTTEGRVYESDL 823
QY 826 LNLSPVGAKFVQAGIGSYTTDLSGFVSDVYRNNPOSTATLWNSPDSWKIRGNLSRQ 885
D 824 LNVSVPIGIKPEKLSYGERSAYDLTLMYIIPDYRRNPSQMTGLAINDVSWLTATNLAHQ 883
QY 886 AFLRGSNNVYVNSNCELFGHYAMELRGSSRYNVNDVGTKLRF 928
D 884 AFIYRAGNHIALTSGVEMFSGQFELRSSSRNRYNDLGAKAVF 926

```

# RESULT 11

ABB98228 standard; protein; 926 AA.

AC ABB98228;

DT 29-AUG-2003 (revised)

DT 03-OCT-2002 (first entry)

DE Chlamydia polypeptide SEQ ID NO 57.

KM Chlamydia; antibacterial; vaccine; immune response; infection.

OS Chlamydia caviae.

PN WO200247718-A2.

PD 20-JUN-2002.

PF 17-DEC-2001; 2001WO-US048773.

PR 15-DEC-2000; 2000US-0255839P.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Johnston SA;

DR WPI; 2002-583472/62.

DR N-PSDB; ABQ78033.

PT Vaccine useful for immunizing an animal, comprising at least one polynucleotide having a Chlamydia sequence or at least one Chlamydia antigen.

PS Claim 21; Page 168-171; 183pp; English.

XX The invention relates to a vaccine (I) comprising at least one polynucleotide (ABQ78008-ABQ78039) having a Chlamydia sequence or at least one Chlamydia antigen (ABB98203-ABB98234) and a pharmaceutically acceptable carrier. The antigens are useful for immunizing an animal, by providing at least one Chlamydia antigen or its antigenic fragment to the animal, in an amount effective to induce an immune response in the animal e.g. mammals including bovine or human. The method is effective to induce an immune response against C. psittaci, C. pneumoniae or non-Chlamydia infection. The method further involves administering to the animal an antigen or an antigenic fragment from Chlamydia species other than C. psittaci or C. pneumoniae or an antigenic fragment from a non-Chlamydia species. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 926 AA;

Query Match 37.7%; Score 1802; DB 5; Length 926;

Best Local Similarity 40.8%; Pred. No. 4,6e-110;  
 Matches 385; Conservative 172; Mismatches 354; Indels 32; Gaps 15;

```

QY 1 MKTSIPWLVSSVLA--FSCHLQSLANBELSPDPSFNGNIDSGTFTPKTSAT--YS 54
D 1 MRBPLYKILISSTLTPLISFHSQLEHVALTGESIIDAN---GAFSPQSTSTAGGTIYN 57
QY 55 LTGDFVFEYEPGKPTLSDSCFKQTTDNLTFLNGHSLTFEFDAGTAGAAAATTANKL 114
D 58 VESDISIVDVQGTAAALASSAFVQJADNLTFRGNHSLISTANAGANPAGINVTADKIL 117
QY 115 TFSGFSLSFDPSSSTVTYTGQGTLSAGVNLNIRKLVVAGNFTADGAIKGSFLL 174
D 118 TLTFPSKLSFKECPSSLVNTGKAMKSGGALNANNSILFDQVYSAENGALISCKAFSL 177
QY 175 TGTSGDALFSNNSSTKGAIAATTAGARIANNQGVYFPLSIASTGAIIDEGTSLSN 234
D 178 TGSSKEISFTTNSSTAKKGAIAATGIAHLSDNQGTIFSGNTAVNSGAVYSEASMTIAG 237
QY 235 NKFLYFEGNAAKTT---GGAICNTKASGSPDLIISNNKTLIPASNAVETSGAIIHAKL 290

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Db      178 TGSSKEISFTNTAKKGAIATGIAHLSDNQITRFSQNTAVNSGAVYSEASMTIAG 237
Qy      235 NKPLFYEGNAKKT-----GCAICNTKASGSPELLISNNKTLIPASNAEISGAIHAKKL 290
Db      238 NNHVAFFNNNAVSGSDCCGAIHCKSGASPTLTIRNKVILFEENISAKGAIYIDKL 297
Qy      291 ALSSGCTEFLLRNNAVSSATPKGAIISIDAGELSLSAETGNTITVRNTLTITTSGSTDTPKR 350
Db      298 ILTSGCTAFIINNVYTHATPKGAIIGTANEGCELTJHEGDIIT-DNNLWATQOMATIKR 356
Qy      351 NAINIGNGKFTELRAAKNHTIFPYDPTISEGSSDVYKINNGSAGALNPYQGTILFSGE 410
Db      357 NAINIEGNGKFTVLRASAGKTIISFYDPTVEGNADLTITLKABGD-KTYNGRIIFSGE 414
Qy      411 TLTDELKVDNKNSSFTQPVLSLGGKLLLOKGYLTLESSTPSQAGSLIGMDSTLTSTT 470
Db      415 KLTEQAAVADVNDKLTFTPTPTTLAAGELVLSGVEVEKTVVQFASGLIIMDACTKLISAK 474
Qy      471 AGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDOLF 530
Db      475 TEDATLTNLAINPTLDGKFAVDAVAAGKNTVLSAIGVIDPTGKFEYHKKLNDTLAL 534
Qy      531 SLKITYDADVDYDINVDISLLIPVPAEDPNSFYGGQGMNVNMTDTATNTKEATA--TWT 588
Db      535 GGIGLSGKGV-TTNNVSHVGVAE--THYGYQGMVSVGMVKNNSDPKTOYAIPTWN 590
Qy      589 KTGVPSPERKSALVNTLMQVFTDINSLOQLVEIGATG-MEHQGFQWVSMTNPLKGTG 647
Db      591 KTGVPSPERRAPVLSLWGSFTIDENSIQVLEIRSVDSILETRGLWVSGIGNPFHKDR 650
Qy      648 D-ENRKGFRRHSGGVVIGSAAHTPKDDLFTFAFCHLFARDKDCFLAHNNSRTYGTLPFK 706
Db      651 NAEKRR-FRHSISGVGLGATINTSREBLSVAFCQLFAKDDYLVSKNAANVAVGSYYQ 709
Qy      707 HSHTLQPNVYRLGRPAKFSESAIEKPREIPLADVOVFSHSDNRMETHYSLPESBGS 766
Db      710 HVSFKFDLTRLPNG----PNTCCSGFSKEIPIFLDAQITTYCHTANNMTSTYDPEVYGS 765
Qy      767 WSNECIAGIGLDLPF-VLSNPHLPKFTIPQMVEVMYVSONSPRESSGRRGFSIGRL 825
Db      766 WGNPTLGLTISTVPIPVFSS--SIFDSYAPFAKIQVVAHQDDPKETTTGGRVPESSDL 823
Qy      826 LNLISIPVAKFVQGDIGSYTYDLSGFVSDVYRNPNPOSTATLVMSPDPMKIRGCNLSRQ 885
Db      824 LNVSVPIQIKFEKLSYGRSAVDLTWYIRPDVYRNPNSCMTGLAINDVSWLTATNLARQ 883
Qy      886 AFLLRGSNNVYVNSNCELFGHYAMELRGSSRNRYVDVGTKLRF 928
Db      884 AFIVRAGNHIALTSGVEMFSGQFGFELRSSRNRYVDLGAKVAF 926

RESULT 13
ABB90542
ID      ABB90542 standard; protein; 928 AA.
XX      ABB90542;
AC      ABB90542;
XX      29-AUG-2003 (revised)
DT      29-JUN-2002 (first entry)
XX      Chlamydia pneumoniae cpe731 protein, SEQ ID NO:33.
DE      Chlamydia pneumoniae cpe731 protein, SEQ ID NO:33.
XX      Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW      human respiratory disease; cardiovascular disease; atherosclerosis;
KW      coronary artery disease; carotid artery stenosis; myocardial infarction;
KW      cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW      strain CML029.
XX      Chlamydia pneumoniae.
OS      Chlamydia pneumoniae.
XX      Key Location/Qualifiers
FH      Peptide 1..26
FT

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FT      /label= Signal_peptide
FT      Protein 27..928
FT      /note= "Mature protein"
XX      MO200202606-A2.
XX      10-JAN-2002.
XX      03-JUL-2001, 2001MO-IB001445.
XX      03-JUL-2000, 2000GB-00016363.
XX      11-JUL-2000, 2000GB-00017047.
XX      21-JUL-2000, 2000GB-00017983.
XX      07-AUG-2000, 2000GB-00019368.
XX      18-AUG-2000, 2000GB-00020440.
XX      14-SEP-2000, 2000GB-00022583.
XX      10-NOV-2000, 2000GB-00027549.
XX      22-DEC-2000, 2000GB-00031706.
XX      (CHIR-) CHIRON SPA.
XX      Ratti G, Grandi G;
XX      WPI, 2002-154726/20.
XX      DR N-PSDB; ABL91200.
XX      Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT      medicament for treatment or prevention of infection due to Chlamydia,
PT      preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX      Claim 1; Page 57; 364pp; English.
XX      Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
XX      pneumoniae (strain CML029), and ABL91184-ABL91373 represent DNA encoding
XX      them. The proteins are predicted to be immunogenic and may therefore be
XX      useful in vaccine production and for diagnostic purposes. Chlamydia
XX      pneumoniae is a common cause of respiratory disease in humans, and is
XX      also involved in the development of cardiovascular diseases such as
XX      atherosclerosis, coronary artery disease, carotid artery stenosis,
XX      myocardial infarction, cerebrovascular disease, aortic aneurysm,
XX      claudication and stroke. The proteins and nucleic acids of the invention
XX      may be used in vaccines and pharmaceutical compositions for the
XX      prevention or treatment of Chlamydial infections, particularly Chlamydia
XX      pneumoniae infections. The proteins may also be used in the detection of
XX      Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
XX      DNA probe assay or blotting techniques for determining Chlamydia
XX      pneumoniae gene expression. The present sequence represents a
XX      specifically claimed Chlamydia pneumoniae protein of the invention.
XX      (Updated on 29-AUG-2003 to standardise OS field)
XX      SQ Sequence 928 AA;

Query Match 37.5%; Score 1794; DB 5; Length 928;
Best Local Similarity 42.7%; Pred. No. 1.5e-109; Index 38; Gaps 17;
Matches 404; Conservative 152; Mismatches 353;

Qy      1 MKTSIPWLVSSVYAFSCHDQ----SIANEELSPDPSFGNIDSGFTP-----KTSAT 51
Db      1 MKSILHWFLLISSSLALPLSLNFGAFAVAVEINLGPNTSFGS---PGYTPPAQTNAQGT 57
Qy      52 TYSITGDVPFPEPKGTPLSDSCFKQTTDNLTVLQNGHSLTFPGFIDAGTHAGAASTTAN 111
Db      58 IYVLTGDSITNAGSPALTPASCFKETTGNIISFGHGVCPLQNDIDAGANC-TFTYTAAN 116
Qy      112 KNLTFSGFSLSPDSSSTVTVTGQGTLSAGGVNLENIKLVVAGNFSRADGAIKAGS 171
Db      117 KLSLFSFSFYSLSL-IQYTAATGTGAIKSTGACSIQSNYSYCFGQNFSDNGALQGS 174
Qy      172 FLTGTGDLFNSNNSSTGCAIATAGARIANNVTGYVFLSNIASTSGAIDDEGTSI 231
Db      175 ISLS-INPNLTFAKNTKQKAGALYSTGCTITNTLNSASFSENTAANGAIYTEASSF 233
Qy      232 LSNKKFLYEGN--AAKTTGAI-CNTKASGPELLISNNKTLIPASNAEISGAIHA 287

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[illegible]

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FT /note= "Specifically claimed in claim 12"  
FT 361. .390  
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FT /note= "Specifically claimed in claim 12"  
FT 365. .373  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
FT 369. .375  
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FT 370. .378  
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FT /note= "Specifically claimed in claim 12"  
FT 381. .398  
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FT /note= "Specifically claimed in claim 12"  
FT 383. .391  
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FT 398. .406  
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FT 412. .425  
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FT 413. .421  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
FT 436. .465  
FT /label= epitope

FT /note= "Specifically claimed in claim 12"  
FT 436. .444  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
FT 443. .451  
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FT /note= "Specifically claimed in claim 12"  
FT 450. .458  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
FT 451. .465  
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FT /note= "Specifically claimed in claim 12"  
FT 454. .462  
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FT 470. .478  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
FT 485. .493  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
FT 487. .496  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
FT 488. .496  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
FT 489. .498  
FT /label= epitope  
FT /note= "Specifically claimed in claim 12"  
  
Query Match 37.5%; Score 1794; DB 9; Length 928;  
Best Local Similarity 42.7%; Pred. No. 1.5e-109;  
Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;  
  
Qy 1 MKTSPWLVSVLAASCHQ---SLANEELSPDDSPFNIDSGTFP-----KTSAT 51  
Db 1 MKSLHMFLLSLALPLSLNPSAFAVEINLGNPSFG---PQTYPPAQTNNADGT 57  
52 TYSLTGDPFPERYBKGKTPSDSCFKOTDNLTFPLNGHSLTFPGFIAGTHAAGAASTTAN 111  
58 IYNLGDVSTTNAGSPFALTAGCFKETTGNLSQGHGYOCLLONIDAGANC-TFTYTAAN 116  
Qy 112 KNLTFSGFSLSPDSSPITVTGQTLSPAGVNDENIRKLVVAGNFSTADGAIKGAS 171  
Db 117 KLSFGSFYSL--IQTNATTGTGAKSTGACSIQSNVSCYFGQNFSDNGALQGS 174  
Qy 172 FLITGTSGDLFESNNSSTGCAIATTAGARKIANNNGYVRELFENINASTSGAIDDEGTST 231  
Db 175 ISLS-LNPNLTFAKNATQKGLYSTGITTINNTLNSAFSENTAANGALYTEASSF 233  
Qy 232 LSNKKFLYPEGN---AKTGGAI-CNTKASGPELIISNNKTLIFASNVAEISGAIIHA 287  
Db 234 ISSNKALSPFNNSVLTATSGAIVCSSTSPAPVLTLSNGELNFTGNATISGAIYT 293  
Qy 288 KKLALSSGFTFEELRN--VSSATPKGALSIDASGELSSEATGNTTFVNTLT--TGST 345  
Db 294 DNLVLSGGRFTLFRNNSAIDTAAPLGAIALAAGSLSLALGDITFEBENTVVKAGSS 353  
Qy 346 DTPKRNAINIG-SNGKTEBLPAKNHTIPFYDPTSEGS--SDVLKINNGSGALNPIQ 402  
Db 354 QTTTRNSINIGNTAKIVQLRASQGNITFYDPTTISITLALDANLNPDLAAGPAYQ 413  
Qy 403 GTILFSGETLTADBLKXADNLKSSFPQVSLSGKLLQGVTLSESTFSQAGSLIGMD 462  
Db 414 GTIVFSGEKSEBAADNLKSTIQPLTAGQSLSGSVTLVASFSQSGESTLMD 473  
Qy 463 SGTTLSTAGSITITNLGINVDSIGLKQPVSLTAKGANKVIYSGKLNLIIDIEGNIYESH 522  
Db 474 AGTTLERADG-ITINNLVAVNVDLSKETKATLAKATQASQVVTLSGSLVDPSGVYEDV 532  
Qy 523 MFSHDQLFSLKITTVDADVDVTNVDISLLIPVPAEDPNSERYFGQGNVNMWTTDTATNKE 582

|    |     |  |     |
|----|-----|--|-----|
| Db | 533 | SWNNPQVFSCLTLLT--ADDPANHITDILADPLEKNPIHMGVQGNWALMSWGEDATATSKSA | 590 |
| Qy | 583 | ATATWTTGTVSPSPERSALVCNTLTMGVFTDRIQLQOLVEIGATSMKHKOGFWMTSMTNF   | 642 |
| Db | 591 | ATLTWTTGTNPENPERGTLVANTLWMTGSDVDVRSIQQLATKVRQSQSTRGICWEGEISNF  | 650 |
| Qy | 643 | LHKTDENRGKGFHTSGGVYIGGSAHTPPDOLFTEAFCHLFARDKDFEIANNSRTYGGT     | 702 |
| Db | 651 | FHKDSTKINGFPHIISAGYVGAHTTLASDNLITAAFCQLPKCKDDHFINNKRASATAAS    | 710 |
| Qy | 703 | LFFKGSHTLQPNQYLRLGRAKFSESAIEKPREIPALADVQVFSHSDNRMETHYTSLPE     | 762 |
| Db | 711 | LHIQHLLATLSSPSLKY--LPSES-----EQPLVPAQASIVYSIKMTKTKYTTQAPK      | 764 |
| Qy | 763 | SEGSMWSNECTIAGGIGLDLPFLVLSNPHLPKFTIPIQMKYEMVYVSONSFESSSD-GRGFS | 821 |
| Db | 762 | GESSWYDGCALBELASSLPHTALSHEGLPFAHVFPFIKYEASVYIHQDSFKERNLTLVRSFD | 821 |
| Qy | 822 | IGRLLSLTVGAKFVQAGDIGDSYYTDLSGFVSDVYRNNPOSTATLVMSPDSWKIRGN      | 881 |
| Db | 822 | SGDLINVSVPICITFRFSRNERASYEAVIVIVADYVRNPPCTALLINNTSMKTTGTN      | 881 |
| Qy | 882 | LSRQAFILRRSNNVYVNSNCELFGHYAMLRRSSRRNVADVETKLRF                 | 928 |
| Db | 882 | LSRQAGIGRAGIFYAESPNILEVYNSLMSIRGSSSYADLGGKQF                   | 928 |

|    |   |
|----|---|
| XX | RESULT 15   |
| XX | AAW88423  |
| XX | ID AAW88423 standard; protein; 928 AA.                                    |
| XX | AAW88423;   |
| XX | AC  |
| XX | AAW88423;   |
| XX | 17-OCT-2003 (revised)   |
| XX | 26-APR-1999 (first entry)   |
| XX | Chlamydia pneumoniae surface exposed protein Omp10.                       |
| XX | Omp10; outer membrane protein 10; surface exposed protein; antigen;       |
| XX | infection; diagnosis; vaccine; atherosclerosis; asthma.                   |
| XX | Chlamydia pneumoniae.   |
| XX | MO9858953-A2.   |
| XX | 30-DEC-1998.  |
| XX | 19-JUN-1998; 98MO-DK000266.   |
| XX | 23-JUN-1997; 97DK-00000744.   |
| XX | (BIRK/) BIRKELUND S.  |
| XX | (CHR/) CHRISTIANSEN G.  |
| XX | Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;               |
| XX | WPI; 1999-105610/09.  |
| XX | N-PSDB; AAX06882.   |
| XX | Species-specific test for identifying mammals infected with Chlamydia     |
| XX | pneumoniae - comprises detecting antibodies specific for outer membrane   |
| XX | proteins of C. pneumoniae or nucleic acids encoding these proteins.       |
| XX | Claim 7; Page 60-62; 115pp; English.                                      |
| XX | This polypeptide comprises the novel 98.4 kDa surface exposed protein     |
| XX | Omp10 of the human respiratory pathogen Chlamydia pneumoniae. Its amino   |
| XX | acid sequence was deduced from DNA (see AAX06882) isolated from a C.      |
| XX | pneumoniae expression library. The invention provides 12 novel surface    |
| XX | exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid          |
| XX | sequences encoding them (see AAX06816-27). A new species specific test is |
| XX | claimed that is used to identify mammals (including humans) infected with |
| XX | Chlamydia pneumoniae.   |

Chlamydia pneumoniae. The test comprises detecting antibodies specific for OmpA-OmpD5 or detecting nucleic acid fragments encoding these outer membrane proteins, especially by PCR. The proteins are also used in the diagnosis of C. pneumoniae infection in mammals. The nucleic acids and proteins can also be used in the immunization of mammals, the nucleic acids being particularly useful as DNA vaccines for effecting in vivo expression of antigens. The vaccines may also prevent atherosclerosis and bronchial asthma, which are possibly associated with C. pneumoniae. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 928 AA:

Query Match 37.5%; Score 1793; DB 2; Length 928;

Best Local Similarity 42.0%, Local NC: 41.0% (20)  
Matches 403; Conservative 153; Mismatches 353; Indels 38; Gaps 17;

QY 1 MKTSPWLVSSVLAFSCHLQ-----SLANEELSPDDSFNGNIDSGTTP-----KTSAT 51

Db 1 MKSSLHWFVISSSLALPLSLNFSAFAAVEINLGPTNSFSG---PCTYTPPAQTINADGT 57

QY 52 TYSLTGDFVFYEYEPGKGPLSDSCFKQTNDNLTFELNGHSLTFGGIDAGTHAGAASTTAN 111

Db 58 IYNLTGVSITNAGSPALTASCFKETGNSFQGHGYQELLQNDAGANC-TFTNTAAN 116

QY 112 KNLTFSGFSLSFDSSPSTVTITGGTILSSAGVNLNIRKLVAGNFSTADGAIKGS 171

Db 117 KLSFGFSYSL-IQTNATGTGAIKSTGACSIQSNYSCYFGQNFSDNGGALQSS 174

QY 172 FLTGTS DALFSNNSSSTKGA IATTAGARIANTGYVRFLSNIASTSGAIDDEGTSI 231

Db 175 ISLS-LNPNTFAKNKATQKGALYSTGGITINNNTLSASFSENTAANGGAIYTEASSF 233

232 LSNKFLYFEGN--AAKTGGAICNTKASGSPELISNNKTLIFASVAETSGAIIHA 287

Db 234 ISSNKAISFINNSVTATSATGGAICYSSSTAPKPVLTLSDNGEINFIGNTAITSGAIYT 293

288 KKLALSSGGFTEFLRNN-VSSATPKGAISIDASGELSLSAETGNITFVRNTLTT-TGST 345

Db 294 DNLVLSSGGPTLFKNNSAIDTAAPLGGAIAIADSGSLSLALGGDITFEQNTVVKGASSS 353

346 DTPKRNAINIG-SNGKFTELRAKNTTFFYDPITSEGT--SDVLKINNGSAGALNPYQ 402

Db 354 QTTTRNSINIGNTNAKI VQLPASQNTI YFYDPITTNHTALSDALNLNGPDLAGNPAYQ 413

403 GTILFSGETLTADLKVADNLKSSFTQPVSLSGKLLQKGVTLLESTSFQEA G SLLGMD 462

Db 414 GTIVFSGEKLSEAEAAEADNLKSTIQQLTLGGQLSLKSGVTLVAKSFSQSFGSTLLMD 473

463 SGTTLSTAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKLLIDIEGNIYESH 522

Db 474 AGTTLETADG-ITINNVLNVDSLKETKKATLKATQASQTVTLSSGLSLVDPGNGVYEDV 532

QY 523 MFSDQLFSLKITVDADVDTNVDISSLIPVPAEDPNSEYGGOGQWNVNWTDTATNTKE 582

Db 533 SMNPNQVFSCLTLT--ADDPANIHTDLADPLEKNPIHWGYQGNNALSWQEDTATKSKA 590

583 ATATWTKTGFVSPERKSALVCNTLWGVFTDIRSLQQLVEIGATGMEHKQGFVSSMTNF 642

Db 591 ATLTWTKGYNPNERGTLVNTLWGSFVDVRSIQQLVATKVRQSQETRGIMCEGISNF 650

643 LHKTDENRKGFRTSGGYVIGGSAHTPKDDLFTFAFCHLFARDKDCFIAHNSRTYGGT 702

Db 651 FHKDSTKINGFRHISAGYVGATTTLASDNLITAAFCQLFGKDRDHFINKNRASAYYAS 710

703 LFFKHSHTLPQNYLRLGRAKSESATIEKFPREIPLALDVQVSFSHSDNRMETHYTSLE 762

Db 711 LHLQHLATLSSPSLLRY--LPGSES-----EQPVLFDAQISYISKNTMTKTYTQAPK 761

QY 763 SEGWSNECIAGGIGLDLPVLSNPHPLFKTFIPQMKVEMVVSQNSFFESSD-GRGFS 821

Db 762 GESSWYNDGCALELASSLPHTALSHGGLFHAYFPFIKVEASYIHQDSFKERNTTLVRSFD 821

QY 822 IGRLLNLSIPVGAKFVQDIDGDSYTYDLSGFFVSDVYRNNPQSTATLVMSPPSWKIRGN 881

Mon Nov 28 09:39:53 2005

us-09-446-677b-2.rag

**Page 16**

Db 822 SGDLINVSVIGTIFERPSFENEASIEAVIIVYADYRKNPDCTALLINNTSKTTGTN 881  
 Qy 882 LSRQAFLLRGSNNVYVNSNCELFCHAMELRGSSRRNVYVGTKLRF 928  
 Db 882 LSRQAGIGRAGIIFYAFSPNLEVTNSNLSMEIRRSSSYNADLGKQKF 928

Search completed: November 25, 2005, 14:10:21  
Job time : 113.98 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: November 25, 2005, 14:02:05 ; Search time 24.1039 Seconds  
(without alignments)  
3704.345 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 4782

Sequence: 1 MKTSIPWLVSSVLAFLSFL.....MELRGSSRNVDVGTGLRF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR 80: \*  
2: pir1: \*  
3: pir2: \*  
4: pir3: \*  
5: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description               |
|------------|--------|-------------|--------|----|---------------------------|
| 1          | 4782   | 100.0       | 928    | 2  | D72077 polymorphic outer  |
| 2          | 4782   | 100.0       | 928    | 2  | H86546 polymorphic outer  |
| 3          | 4782   | 100.0       | 949    | 2  | F81591 polymorphic membra |
| 4          | 1794   | 37.5        | 928    | 2  | B72077 polymorphic membra |
| 5          | 1794   | 37.5        | 928    | 2  | B86546 polymorphic outer  |
| 6          | 1785   | 37.3        | 928    | 2  | G86546 polymorphic outer  |
| 7          | 1785   | 37.3        | 928    | 2  | G81591 polymorphic membra |
| 8          | 1763   | 36.9        | 930    | 2  | D86546 polymorphic outer  |
| 9          | 1763   | 36.9        | 930    | 2  | A81591 polymorphic membra |
| 10         | 1761   | 36.8        | 930    | 2  | D72078 polymorphic outer  |
| 11         | 1734   | 36.3        | 936    | 2  | C72078 polymorphic outer  |
| 12         | 1733   | 36.2        | 936    | 2  | B81591 polymorphic membra |
| 13         | 1733   | 36.2        | 936    | 2  | C86546 polymorphic outer  |
| 14         | 1591   | 33.3        | 772    | 2  | H86492 Pmp_3 [imported] - |
| 15         | 1435.5 | 30.0        | 841    | 2  | E72130 polymorphic membra |
| 16         | 1353   | 28.3        | 922    | 2  | B72131 polymorphic outer  |
| 17         | 1353   | 28.3        | 922    | 2  | B86491 polymorphic outer  |
| 18         | 1352   | 28.3        | 922    | 2  | F81539 polymorphic membra |
| 19         | 1284.5 | 26.9        | 973    | 2  | B86547 polymorphic outer  |
| 20         | 1284.5 | 26.9        | 973    | 2  | F72076 polymorphic outer  |
| 21         | 1284.5 | 26.9        | 995    | 2  | C81593 polymorphic membra |
| 22         | 1203   | 25.2        | 1276   | 2  | B86546 polymorphic membra |
| 23         | 1203   | 25.2        | 1276   | 2  | C81591 polymorphic outer  |
| 24         | 1164   | 24.3        | 712    | 2  | B86492 polymorphic membra |
| 25         | 1144.5 | 23.9        | 1407   | 2  | B72078 polymorphic outer  |
| 26         | 1102.5 | 23.1        | 1013   | 2  | G71460 probable outer mem |
| 27         | 1040   | 21.7        | 987    | 2  | H81722 polymorphic membra |
| 28         | 843.5  | 17.6        | 494    | 2  | D86493 polymorphic outer  |
| 29         | 837    | 17.5        | 878    | 2  | B71460 probable outer mem |

|    |       |      |      |   |                           |
|----|-------|------|------|---|---------------------------|
| 30 | 831.5 | 17.4 | 427  | 2 | A86493 polymorphic outer  |
| 31 | 829.5 | 17.3 | 867  | 2 | F81721 polymorphic membra |
| 32 | 790   | 16.5 | 445  | 2 | B86493 Pmp_5 [imported] - |
| 33 | 736.5 | 15.4 | 359  | 2 | C86493 Pmp_4 [imported] - |
| 34 | 679.5 | 14.2 | 947  | 2 | D72067 polymorphic membra |
| 35 | 678.5 | 14.2 | 947  | 2 | G86557 polymorphic membra |
| 36 | 610.5 | 12.8 | 964  | 2 | E71460 probable outer mem |
| 37 | 610.5 | 12.8 | 1723 | 2 | B86557 polymorphic membra |
| 38 | 610.5 | 12.8 | 1723 | 2 | E72067 polymorphic membra |
| 39 | 610.5 | 12.8 | 1732 | 2 | B81601 polymorphic membra |
| 40 | 608.5 | 12.7 | 978  | 2 | C86547 polymorphic outer  |
| 41 | 608.5 | 12.7 | 978  | 2 | B81593 polymorphic membra |
| 42 | 604.5 | 12.6 | 986  | 2 | B81675 polymorphic membra |
| 43 | 604   | 12.6 | 1016 | 2 | H71460 probable outer mem |
| 44 | 603.5 | 12.6 | 978  | 2 | G72076 polymorphic outer  |
| 45 | 600.5 | 12.6 | 934  | 2 | G86548 polymorphic outer  |

## ALIGNMENTS

## RESULT 1

D72077 polymorphic outer membrane protein g family - Chlamydia pneumoniae (strain CWL029)

C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004

C/Accession: D72077

R/Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A/Reference number: A72000; PMID:99206606; PMID:10192388

A/Accession: D72077

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-928 <ARN>

A/Cross-references: UNIPROT:O86164; UNIPARC:UPI000002FFEF; GB:AE001628; GB:AE001363; NID:

A/Experimental source: strain CWL029

C/Genetics:

A/Gene: pmp\_11

C/Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

| Query Match           | 100.0% | Score 4782   | DB 2 | Length 928                      |
|-----------------------|--------|--|------|---------------------------------|
| Best Local Similarity | 100.0% | Pred. No. 1.5e-261   |      |                                 |
| Matches               | 928    | Conservative   | 0    | Mismatches 0; Indels 0; Gaps 0; |
| QY                    | 1      | MKTSIPWLVSSVLAFLSFL.....MELRGSSRNVDVGTGLRF 60                  |      |                                 |
| DB                    | 1      | MKTSIPWLVSSVLAFLSFL.....MELRGSSRNVDVGTGLRF 60                  |      |                                 |
| QY                    | 61     | FYEPGKTPLDSCFPKQTTDNLTFLNGHSLTFGFIDAGTHAGAAATTANKRLTFSGFS 120  |      |                                 |
| DB                    | 61     | FYEPGKTPLDSCFPKQTTDNLTFLNGHSLTFGFIDAGTHAGAAATTANKRLTFSGFS 120  |      |                                 |
| QY                    | 121    | LISFDSPTTYYTGGGLTSSAGVNLIRKLVAAGNFSTADGAIKCAFLTGTSGD 180       |      |                                 |
| DB                    | 121    | LISFDSPTTYYTGGGLTSSAGVNLIRKLVAAGNFSTADGAIKCAFLTGTSGD 180       |      |                                 |
| QY                    | 181    | ALFSNNSSSTKGALATTGARIANTGYRFLSNIASTSGAIDDEGSIISNNFLVF 240      |      |                                 |
| DB                    | 181    | ALFSNNSSSTKGALATTGARIANTGYRFLSNIASTSGAIDDEGSIISNNFLVF 240      |      |                                 |
| QY                    | 241    | EGNAATTGCAICNTKASGPELISNNKTLIFASVNAETSGAIIHAKKLALSSGFTEF 300   |      |                                 |
| DB                    | 241    | EGNAATTGCAICNTKASGPELISNNKTLIFASVNAETSGAIIHAKKLALSSGFTEF 300   |      |                                 |
| QY                    | 301    | LNNVSSATPKGALSIDASGELISAETGNTTFVRNTLTGGSTDTPPKRNAINISNGK 360   |      |                                 |
| DB                    | 301    | LNNVSSATPKGALSIDASGELISAETGNTTFVRNTLTGGSTDTPPKRNAINISNGK 360   |      |                                 |
| QY                    | 361    | FTELRAKNTTIFPDPTISSEGTSDVLKINNGSAGALNPGYGTILFSGETTLTADLKVA 420 |      |                                 |
| DB                    | 361    | FTELRAKNTTIFPDPTISSEGTSDVLKINNGSAGALNPGYGTILFSGETTLTADLKVA 420 |      |                                 |

QY 421 DNKSSFTQPVSLSGKLLQKGVLTLESTSFSGEASLLGMDSGTLLSTAGSITTTNLG 480  
|  
|  
|  
Db 421 DNKSSFTQPVSLSGKLLQKGVLTLESTSFSGEASLLGMDSGTLLSTAGSITTTNLG 480  
QY 481 INVDSLGKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITYVDAD 540  
|  
|  
|  
Db 481 INVDSLGKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITYVDAD 540  
QY 541 VDTNVDISLLIPVAEDPNSSEYFQOGQNNVMTTDTATNTKEATATATWTGTGFPVSPERKS 600  
|  
|  
|  
Db 541 VDTNVDISLLIPVAEDPNSSEYFQOGQNNVMTTDTATNTKEATATATWTGTGFPVSPERKS 600  
QY 601 ALVCNTLMGVFTDTRSLQQLVEIGATGMEHKQFWSSMTNLFHKTGDENRKGFRTSSGG 660  
|  
|  
|  
Db 601 ALVCNTLMGVFTDTRSLQQLVEIGATGMEHKQFWSSMTNLFHKTGDENRKGFRTSSGG 660  
QY 661 YVIGGSATHTPKDDLPTFAFCHLFPARDKCFIAHNNSTRYGGTLFPKHSHTLQPNYLRLG 720  
|  
|  
|  
Db 661 YVIGGSATHTPKDDLPTFAFCHLFPARDKCFIAHNNSTRYGGTLFPKHSHTLQPNYLRLG 720  
QY 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSMNECTIAGIGLDL 780  
|  
|  
|  
Db 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSMNECTIAGIGLDL 780  
QY 781 PFVLSNHPHLPKFTIPLQMKVEMVYVYVSSQNSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
|  
|  
|  
Db 781 PFVLSNHPHLPKFTIPLQMKVEMVYVYVSSQNSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
QY 841 IGDSTYTDLSGFPVSDVYRNNPOSTATLVMSPDWKIRGKULSROAFLLRGNNYVYNSN 900  
|  
|  
|  
Db 841 IGDSTYTDLSGFPVSDVYRNNPOSTATLVMSPDWKIRGKULSROAFLLRGNNYVYNSN 900  
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928  
|  
|  
|  
Db 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

RESULT 2  
H86546  
polymorphic outer membrane protein G family [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H86546  
R:Shirai, M.; Hixkawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: A86491; PMID:20330349; PMID:10871362  
A:Accession: H86546  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-928 <STO>  
A:Cross-references: UNIPROT:086164; UNIPARC:UP1000002FFBF; GB:BA000008; NID:g8978822; PI  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: pmp\_11  
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 100.0%; Score 4782; DB 2; Length 928;  
Best Local Similarity 100.0%; Pred. No. 1.5e-261;  
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSLPWLIVSSVLAFAFCHLQSLANEELSPDPSFNGNIDSGTFTPKTSATTVSLTGDF 60  
|  
|  
|  
Db 1 MKTSLPWLIVSSVLAFAFCHLQSLANEELSPDPSFNGNIDSGTFTPKTSATTVSLTGDF 60  
QY 61 FYEPKGPPLSDCKQKOTTDNLTPFLGNGHSLTFGIDAGTAGAASATTANKNLTFSGFS 120  
|  
|  
|  
Db 61 FYEPKGPPLSDCKQKOTTDNLTPFLGNGHSLTFGIDAGTAGAASATTANKNLTFSGFS 120  
QY 121 LLSPPSSSTTYTTOGTLSSAGVNLNIRKLVVAGNPSADGAGIAGASFLTLGTSGD 180  
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|  
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Db 121 LLSPPSSSTTYTTOGTLSSAGVNLNIRKLVVAGNPSADGAGIAGASFLTLGTSGD 180

QY 181 ALFSSNNSSSTKGGAITTAGARIANNNTGYRFLUSNIASFGAIDDEGTSLSNKFLYF 240  
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Db 181 ALFSSNNSSSTKGGAITTAGARIANNNTGYRFLUSNIASFGAIDDEGTSLSNKFLYF 240  
QY 241 EGNAAKTGGALCNTASGPELISNNKTLFASVVAETSGGAIAKXKLAASSGGFTTF 300  
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|  
|  
Db 241 EGNAAKTGGALCNTASGPELISNNKTLFASVVAETSGGAIAKXKLAASSGGFTTF 300  
QY 301 LRNNVSATPKGGAISIDASGELSLETGNITFVANTLTGTTGTDTPKRNAINISNGK 360  
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|  
Db 301 LRNNVSATPKGGAISIDASGELSLETGNITFVANTLTGTTGTDTPKRNAINISNGK 360  
QY 361 FTFLRAKNTHTFFYPDITSEGTSDVYLKINNSAGALNPQGTILFSGETLTADBLKXA 420  
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|  
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Db 361 FTFLRAKNTHTFFYPDITSEGTSDVYLKINNSAGALNPQGTILFSGETLTADBLKXA 420  
QY 421 DNKSSFTQPVSLSGKLLQKGVLTLESTSFSGEASLLGMDSGTLLSTAGSITTTNLG 480  
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Db 421 DNKSSFTQPVSLSGKLLQKGVLTLESTSFSGEASLLGMDSGTLLSTAGSITTTNLG 480  
QY 481 INVDSLGKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITYVDAD 540  
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Db 481 INVDSLGKQPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITYVDAD 540  
QY 541 VDTNVDISLLIPVAEDPNSSEYFQOGQNNVMTTDTATNTKEATATATWTGTGFPVSPERKS 600  
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Db 541 VDTNVDISLLIPVAEDPNSSEYFQOGQNNVMTTDTATNTKEATATATWTGTGFPVSPERKS 600  
QY 601 ALVCNTLMGVFTDTRSLQQLVEIGATGMEHKQFWSSMTNLFHKTGDENRKGFRTSSGG 660  
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Db 601 ALVCNTLMGVFTDTRSLQQLVEIGATGMEHKQFWSSMTNLFHKTGDENRKGFRTSSGG 660  
QY 661 YVIGGSATHTPKDDLPTFAFCHLFPARDKCFIAHNNSTRYGGTLFPKHSHTLQPNYLRLG 720  
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|  
Db 661 YVIGGSATHTPKDDLPTFAFCHLFPARDKCFIAHNNSTRYGGTLFPKHSHTLQPNYLRLG 720  
QY 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSMNECTIAGIGLDL 780  
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|  
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Db 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSMNECTIAGIGLDL 780  
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Db 781 PFVLSNHPHLPKFTIPLQMKVEMVYVYVSSQNSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
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Db 841 IGDSTYTDLSGFPVSDVYRNNPOSTATLVMSPDWKIRGKULSROAFLLRGNNYVYNSN 900  
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928  
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Db 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

RESULT 3  
F81591  
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C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 15-Jun-2001  
C:Accession: F81591  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heldelberg, J.F.; White, O.; Hickey, J.  
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis Moyn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; PMID:20150255; PMID:10684935  
A:Accession: F81591  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-949 <REA>  
A:Cross-references: UNIPARC:UP100001655FA; GB:AE002192; GB:AE002161; NID:97189226; PIDN:;  
A:Experimental source: strain AR39, HU cells  
C:Genetics:  
A:Gene: CP0302  
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 100.0%; Score 4782; DB 2; Length 949;  
Best Local Similarity 100.0%; Pred. No. 1.5e-261;  
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 FYERKGPVLSDSGCFKOTDNLFTLGNGHSLTFGFIAGTAGAGAAATTNKLTFSGFS 120
DB FYERKGPVLSDSGCFKOTDNLFTLGNGHSLTFGFIAGTAGAGAAATTNKLTFSGFS 141
QY 82 FYERKGPVLSDSGCFKOTDNLFTLGNGHSLTFGFIAGTAGAGAAATTNKLTFSGFS 141
DB FYERKGPVLSDSGCFKOTDNLFTLGNGHSLTFGFIAGTAGAGAAATTNKLTFSGFS 141
QY 121 LLSFSSPSTVTVTGOGTSLSSAGVNLNIRKLVVAGNFSTADGAIKGSFLLTGSGD 180
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QY 142 LLSFSSPSTVTVTGOGTSLSSAGVNLNIRKLVVAGNFSTADGAIKGSFLLTGSGD 201
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QY 202 ALFSSNNSSTKGAIATTAGARIANTGYVFLSNIASTSGAIDEGTSLSNKFLYF 261
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QY 382 FTBLRAKNTHTIFPYDPTITSEGTSDYLKINNGAGALNPYQGITLPSGETTLTADBLKVA 441
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QY 502 INVDSLGLKQVSLTAKGASNKVIVSGKLLNIDIEGNVYESHMSHQLFSLKITVDAD 561
DB INVDSLGLKQVSLTAKGASNKVIVSGKLLNIDIEGNVYESHMSHQLFSLKITVDAD 561
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QY 562 VDTNVDISSLIPVAEDPNSSEYFGQGMVNMVTTDTATNTKEATATVTKGFVPSPERKS 621
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DB ALVNTLMGVPTDTRSLQOLVEIGATGMEHKQGFVWSMTNFKLTGDNKRGFRHTSG 681
QY 622 ALVNTLMGVPTDTRSLQOLVEIGATGMEHKQGFVWSMTNFKLTGDNKRGFRHTSG 681
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QY 661 YVIGSHTPDDLETFAPFCHLFAKDCCFAHNSRTYGGTLFPKSHTLQPNYRLIG 720
DB YVIGSHTPDDLETFAPFCHLFAKDCCFAHNSRTYGGTLFPKSHTLQPNYRLIG 741
QY 682 YVIGSHTPDDLETFAPFCHLFAKDCCFAHNSRTYGGTLFPKSHTLQPNYRLIG 741
DB YVIGSHTPDDLETFAPFCHLFAKDCCFAHNSRTYGGTLFPKSHTLQPNYRLIG 741
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QY 742 RAKSESALIEKPREPILALDVQVFSHSDNRMTHTYSLPESGMSNECIAGIGLDL 801
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DB PFLVLSNHPLEFKTIPQKYMVMYVSONSPFESSDDGSGISGLMLSLPVGAKFYQGD 861
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QY 862 IGDSTYVDSGFFVSDVYRNPOSTATLVMSPDKWIRGNLISOAFLILGSSNNYVNSN 921
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DB CELFGHYAMELRGSSRYNVDVGTCLRF 949
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RESULT 4  
B72077  
polymorphic membrane protein G family CP0306 [imported] - Chlamydomphila pneumoniae (stra

C:Species: Chlamydomphila pneumoniae, Chlamydia pneumoniae  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: B72077; B81592  
R:Klaman, S.; Mitchell, W.; Marache, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: B72077  
A:Molecule type: DNA  
A:Residues: 1-928 <ARN>

A:Cross-references: UNIPROT:Q9Z388; UNIPARC:UPI0000047087; GB:AE001628; GB:AE001363; NID:  
A:Experimental source: strain CML029  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255; PMID:10684935  
A:Accession: B81592  
A:Molecule type: DNA  
A:Residues: 1-928 <REA>  
A:Cross-references: UNIPARC:UPI0000047087; GB:AE002192; GB:AE002161; NID:97189226; PIDN:  
A:Experimental source: strain AR39, HL cells  
C:Genetics:  
A:Gene: pmp\_9; CP0306  
C:Superfamily: Chlamydomphila pneumoniae polymorphic outer membrane protein G

Query Match 37.5%; Score 1794; DB 2; Length 928;  
Best Local Similarity 42.7%; Pred. No. 3e-93;  
Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;

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QY 58 IYVLTGDSVTITNAGSFTALTAISCFKETTGNLSFGHGQYFOLLQNDIAGANC--TFYTAAN 116
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QY 112 KULTFSGFSLSPDSSPSTVTVTGOGTSLSSAGVNLNIRKLVVAGNFSTADGAIKGS 171
DB KULTFSGFSLSPDSSPSTVTVTGOGTSLSSAGVNLNIRKLVVAGNFSTADGAIKGS 174
QY 117 KULTFSGFSLSPDSSPSTVTVTGOGTSLSSAGVNLNIRKLVVAGNFSTADGAIKGS 174
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DB SMNVPQVFCITLT--ADDPANIHITDLAADPLEKXPHIMVGQGNALMDEBTATKSKA 590
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 Db 354 QTKRNSIDIGSTAKITNLRALISGHSIFFYDPIITANTADSTDLNKAADAGNSTDYSG 413  
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 Db 760 AYEPEVSGWGNNAFNMMLGAS-----SHSYPEYLHCFDYAPYIKLNTLYIRQDSFEKG 814  
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 RESULT 7  
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 polymorphic membrane protein G family CP0303 [imported] - Chlamydia pneumoniae (stra  
 C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
 C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C/Accession: G81591  
 R/Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,  
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
 Nucleic Acids Res. 28, 1397-1406, 2000  
 A/Title: Genome sequences of Chlamydia trachomatis Moyn and Chlamydia pneumoniae AK39.  
 A/Reference number: AB1500; MUID:2015025; PMID:10684935  
 A/Accession: G81591  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-928 <REA>  
 A/Cross-references: UNIPROT:Q9R65; UNIPARC:UP1000002FFP0; GB:AE002192; GB:AE002161; NIT  
 A/Experimental source: strain AK39, HL cells  
 C/Genetics:  
 A/Gene: CP0303

C/Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G  
 Query Match 37.3%; Score 1785; DB 2; Length 928;  
 Best Local Similarity 40.4%; Pred. No. 9.5e-93;  
 Matches 385; Conservative 173; Mismatches 344; Indels 52; Gaps 18;  
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 QY 464 GTTLSTAGSITITNLGINVDSLKQPVSLTAKGASNKYIVSGKNTLIDIEGNIYESHM 523  
 Db 474 GTTLKASTEETVLTGLSIPVDSLGEKGVVIASAAKRNVALSGPILLIDNQGAYENHD 533  
 QY 524 FSHDQLFSLKITVDADVDTNVDISLIPPAEDPNSEYGFQOGOMNVNMTTDTAT--NTK 581  
 Db 534 LKKTQDFSPVQLSA-LGTATTTDVPA---VPYATPPTHYGOGTGMGTWVDITASTPKTK 589  
 QY 582 EATATWTKTGVPSPERKALVONTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTN 641  
 Db 590 TATLAWTNTGYLPPNERQGPLVPNSLWGSFSDIOAIGVIERALTLCSDRGFMAAGVAN 649  
 QY 642 FLHKTGDEMRKGRHNSGGVIVIGSATPRKDLFTFAFCHLPARDXCFIAHNNSTPYG 701  
 Db 650 FLDKDKKGRKRYRKHSGGYAIGAAQTCSENLISFAFCQLFSDQKPLVAKNHTDYAG 709  
 QY 702 TLFFKSHHTLOPONYLRLGRAKFSBSAIEKFP---REIPLADVOVYFSHSDRMETHYT 758  
 Db 710 AFIQIHTTEC-----SGFIGCLDLKLGSMHKLPLVLEGQLAYHVSNDLTKYTT 759  
 QY 759 SLPESEGSWSNECIAGIGLDLPVLSNPH---LFTKFIPOMKYEMVYVSONSEFESS 814  
 Db 760 AYEPEVSGWGNNAFNMMLGAS-----SHSYPEYLHCFDYAPYIKLNTLYIRQDSFEKG 814  
 QY 815 SDGRGSIIGLLNLSTIVGAKFVQGDIGSYTYDLSGFVSDYVRNNPOSTATLWNSPDS 874  
 Db 815 TEGRSPDSDNLFNLSLPVIGVKEFKFSDCNDFSYDLTSLVDPDLIRNDPKCTTALVIGAS 874  
 QY 875 WKIRGGLSRQAFLLRGSNNYVYNSNCELFGHYAMELRGSSRNNYNDVGTKLRF 928  
 Db 875 WEYIANNLARQALQVRAGSHYAFSPMEFVLGQFVFEVRGSSRIYNDLGKQGF 928  
 RESULT 8  
 D86546

polymorphic outer membrane protein G family [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 15-Jun-2001  
C/Accession: D86546  
R/Shitai, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is  
Nucleic Acids Res. 28, 2311-2314, 2000  
A>Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
A/Reference number: A86491; MUID:20330349; PMID:10871362  
A/Accession: D86546  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-930 <STO>  
A/Cross-references: UNIPARC:UPI00001655FB; GB:BA000008; NID:98978818; PIDN:BAA9654.1; G  
A/Experimental source: strain J138  
C/Genetics:  
A:Gene: pmp 8  
C/Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 36.9%; Score 1763; DB 2; Length 930;  
Best Local Similarity 41.7%; Pred. No. 1.6e-91;  
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

QY 1 MKTSLPVLVSSVLAFCCHLOSLAN---EELSPDSDPFGNIDSGTTPKTSK---TTY 53  
DB 1 MKTSLPVLVSSVLAFCCHLOSLAN---EELSPDSDPFGNIDSGTTPKTSK---TTY 53  
QY 54 SLTGDVFEYBPGKTPSLDSCFKQTTDNLTFLGNGHSLTFEGIDAGTHAGAASTTANKN 113  
DB 59 VLSGNVYINDAGKGTALTGCCFTETTGDLTFGKGYSPFNVTAGSNAGAASTTADKA 118  
QY 114 LTFSGFSLSPDSSPTVTVTGGCTLSAGGVNLENIRKLVVAGNFTA---DGAIKGA 170  
DB 119 LTFGFSNLSTIAAPGTTVAGSKSTLSAGALNLTNGDTILFSGQVNSNEANNNGAITAK 178  
QY 171 SFLITGSGDALFSNNSSSTKGAIAATTAGRIANNNGYVFLSNIASTSGAIDDEGTS 230  
DB 179 TLSISGNTSSITFTSNSAKKLGAIYSSAAASISGNTGQLVFNNKGETGGALGFPASS 238  
QY 231 ILSNNKFLYFEGNAKTT---GGAICNTKASGPELIISSNNKTLIPASNVETSGAIIHA 287  
DB 239 SITONSSLPFSGNATTAAGKGAIIYCEKTEPTLTISGNKSLTFEANSVTOGGALICA 298  
QY 288 KKLALSGGFTPELRNNV--SSATPKGAISIDSGELSLAETGNTTFVNTLTGSTD 346  
DB 299 HGLDLASAAGPTLFSNNRCGNTAAGKGAIIADSGSLSLSANOGDITFLGNTLTST--SAP 357  
QY 347 TPKRNAINISNGFTELRANKHTTFYDPTISEGT--SSDVLKINNGSAGALNPYQGTI 405  
DB 358 TSTNNAIYLGSSAKITNLRAAGOSIIFYDPIASNTTASDVLTIINPDNSPLDYSGTI 417  
QY 406 LFSGETLTADELKAVADNKKSFPTQVSLSGGKLLQKGVTLSESTFSQEAAGSLGMDSGT 465  
DB 418 VFSGEKLSADEKKAADNFTSLIKQPLALASGTLAKGNVELDVNGFTQTEGSTLLMQPGT 477  
QY 466 TLTSTAGSITTTNLGINVDSLGLKQPVSLTAKGASNKVIYSGKLNLDIEGNIYESHMF 525  
DB 478 KKLADTETASITLKLVDVDSALEGNKSVSIEETAGANKITLTLSPLVFQSSNGFYESTHTI- 536  
QY 526 HDQFLSL-LKTTVDADVDTNVDISLIVPAEDPNSEVFGQGVNNVNTTDTANTYKAT 584  
DB 537 -NQAFTQPLVFTATAASDIYIDALLTSPVQTPPEPHYGOGHWEATV-ADTST--AKSGT 593  
QY 585 AITWTKGVSPERSALVCMTLMGVTFDITSLQOLVLEIGATGMHKGQFVWSVNTNLH 644  
DB 594 MTWTTGTGNPERSASVVPDLSMASFTDIRLQOIMTSQANSIYQOGLAASGTANFFH 653  
QY 645 KTGDENRKGFRHTSGGVYIGSAAHTPKDGLFTFAFCHLFARDKCFIAHNSRTYGGTLF 704  
DB 654 KDKSGTNGAFRHKSGYIVGSAEDPSNHSVACQPLGKDKDLFIYENTSHNYLASY 713  
QY 705 FKHSHTLOPQVNLIRGAKFSESAIEKFPREIPLALDVQVFSHSDNMEHTYLSLPESE 764  
DB 714 LQHRALFG-----GLPMPSPFGSITDMLKDIPILNQLSYSSYKNDMDRRTYSYPEAQ 766

polymorphic outer membrane protein G family CP0307 [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: A81591  
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A/Reference number: A81500; MUID:20150255; PMID:10684935  
A/Accession: A81591  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-930 <REA>  
A/Cross-references: UNIPROT:Q9Z393; UNIPARC:UPI00001655FB; GB:AE002193; GB:AE002161; NID:  
A/Experimental source: strain AR39, HL cells  
C/Genetics:  
A:Gene: CP0307  
C/Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 36.9%; Score 1763; DB 2; Length 930;  
Best Local Similarity 41.7%; Pred. No. 1.6e-91;  
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

QY 1 MKTSLPVLVSSVLAFCCHLOSLAN---EELSPDSDPFGNIDSGTTPKTSK---TTY 53  
DB 1 MKTSLPVLVSSVLAFCCHLOSLAN---EELSPDSDPFGNIDSGTTPKTSK---TTY 53  
QY 54 SLTGDVFEYBPGKTPSLDSCFKQTTDNLTFLGNGHSLTFEGIDAGTHAGAASTTANKN 113  
DB 59 VLSGNVYINDAGKGTALTGCCFTETTGDLTFGKGYSPFNVTAGSNAGAASTTADKA 118  
QY 114 LTFSGFSLSPDSSPTVTVTGGCTLSAGGVNLENIRKLVVAGNFTA---DGAIKGA 170  
DB 119 LTFGFSNLSTIAAPGTTVAGSKSTLSAGALNLTNGDTILFSGQVNSNEANNNGAITAK 178  
QY 171 SFLITGSGDALFSNNSSSTKGAIAATTAGRIANNNGYVFLSNIASTSGAIDDEGTS 230  
DB 179 TLSISGNTSSITFTSNSAKKLGAIYSSAAASISGNTGQLVFNNKGETGGALGFPASS 238  
QY 231 ILSNNKFLYFEGNAKTT---GGAICNTKASGPELIISSNNKTLIPASNVETSGAIIHA 287  
DB 239 SITONSSLPFSGNATTAAGKGAIIYCEKTEPTLTISGNKSLTFEANSVTOGGALICA 298  
QY 288 KKLALSGGFTPELRNNV--SSATPKGAISIDSGELSLAETGNTTFVNTLTGSTD 346  
DB 299 HGLDLASAAGPTLFSNNRCGNTAAGKGAIIADSGSLSLSANOGDITFLGNTLTST--SAP 357  
QY 347 TPKRNAINISNGFTELRANKHTTFYDPTISEGT--SSDVLKINNGSAGALNPYQGTI 405  
DB 358 TSTNNAIYLGSSAKITNLRAAGOSIIFYDPIASNTTASDVLTIINPDNSPLDYSGTI 417  
QY 406 LFSGETLTADELKAVADNKKSFPTQVSLSGGKLLQKGVTLSESTFSQEAAGSLGMDSGT 465  
DB 418 VFSGEKLSADEKKAADNFTSLIKQPLALASGTLAKGNVELDVNGFTQTEGSTLLMQPGT 477  
QY 466 TLTSTAGSITTTNLGINVDSLGLKQPVSLTAKGASNKVIYSGKLNLDIEGNIYESHMF 525  
DB 478 KKLADTETASITLKLVDVDSALEGNKSVSIEETAGANKITLTLSPLVFQSSNGFYESTHTI- 536  
QY 526 HDQFLSL-LKTTVDADVDTNVDISLIVPAEDPNSEVFGQGVNNVNTTDTANTYKAT 584  
DB 537 -NQAFTQPLVFTATAASDIYIDALLTSPVQTPPEPHYGOGHWEATV-ADTST--AKSGT 593  
QY 585 AITWTKGVSPERSALVCMTLMGVTFDITSLQOLVLEIGATGMHKGQFVWSVNTNLH 644  
DB 594 MTWTTGTGNPERSASVVPDLSMASFTDIRLQOIMTSQANSIYQOGLAASGTANFFH 653  
QY 645 KTGDENRKGFRHTSGGVYIGSAAHTPKDGLFTFAFCHLFARDKCFIAHNSRTYGGTLF 704  
DB 654 KDKSGTNGAFRHKSGYIVGSAEDPSNHSVACQPLGKDKDLFIYENTSHNYLASY 713  
QY 705 FKHSHTLOPQVNLIRGAKFSESAIEKFPREIPLALDVQVFSHSDNMEHTYLSLPESE 764  
DB 714 LQHRALFG-----GLPMPSPFGSITDMLKDIPILNQLSYSSYKNDMDRRTYSYPEAQ 766

Db 478 LUKADTEAISLTUKVVDLSALEGKNSVSIETRAGANKTTLTSLPLVFDQSSGNFIESHTI - 536

Qy 526 HDOLFSL-LKITTVDADVDTNDVDSLSLIPVPAEDPENSEYGFQGMVNMVNTDTATVTKEAT 584

Db 537 -NQAFQGLVLPYTAATAASDIYIDALLTSPVQTPERPHYQYGHMEATV-ADTST-AKSGT 593

Qy 585 ATWTKGFVPSPERKSALVCNTLWGVFTDIBSLQOQVBEIGATGMEHKOGFWVSSMNTNELH 644

Db 594 MTWVTGTPNPNPERASVVPDLSMASFIDITLQOIMTSQANSITVQCGIWLASGRANFEH 653

Qy 645 KTGDENRKGPRHTSGYIVIGSSAHTPKDOLFPAFCFLPARDKCFIANNHSRTYGTLEF 704

Db 654 KDKSGTNOAFPHKHSYGYIVIGSSAEDPSENIFSVAFCQFGPKDKOLFIVENTSHNYLASTLY 713

Qy 705 FKHSHTLOPONYLRLGRAKFSESALIEKFPREIPLADVQVSPSHSDNMETHYISLSEPE 764

Db 714 LQHRFAFLG-----GLPMPSGSITDMLKIDPLILNAQLSASYKNDMDRRTYSYSPAQ 766

Qy 765 GSMNSECTAGGIGLDLPFVLSNPNHPLFKTIFPOMKVENVYVYSSONSFFPSSSDGRCFSIGR 824

Db 767 GSWTNSGALBEGSLATYLPKEAPFFQGYPPFLFKQAVYVRQGNFKESGAEARAFDDGD 826

Qy 825 LNLNLSIPFGARFVQGDIDGDTTYDLSGFFVSDVYRNNQOSTATLVMGSDSKIKIGANLSR 884

Db 827 LVNCSIPVIGRIELEKISSEDEKNNFEISLAIYIGVYKRNKRSTSLMVGSGASVTSJCKNLAR 886

Qy 885 QAPLLRGSNNVYVNSNCELPGHYAMELJGSSRNRYVVDVGTCLRF 928

Db 887 QAPLASAGSHLTLSPHVELSGEAAAYELRGSAAHYVVDGGLYSF 930

RESULT 10  
D72078  
polymorphic outer membrane protein g family - Chlamydia pneumoniae (strain CWI029)  
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: D72078  
R/Katman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.  
Nature Genet. 21, 385-389, 1999  
A/Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A/Reference number: A72000; MUID:99206606; PMID:10192388  
A/Accession: D72078  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-930 <ARN>  
A/Cross-references: UNIPROT:Q9Z393; UNIPARC:UPI000004708C; GB:AE001627; GB:AE001363; NII  
A/Experimental source: strain CWI029  
C/Genetics:  
A/Gene: pmp\_8  
Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

[illegible]

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Db 229 SITONSLFPGSNTNTLDAAGKGAICYCEKTGEFPTLTISGNKSLTPRENSVYOGGAIICA 298
OY 298 KKLALSSGGFTEFLANNV-SSATPKGGAISIDASGELSLSAETGNTTFVBNLTITTTGSTD 346
Db 299 HGLDLSAAGPTLFSNNRCGNTAAGKGAIAIADSGELSLSANOGDITFLCNTLTST-SAP 357
OY 347 TPKRAVINGSGKTEFLRAAKNHTFFPYDPTISEGT-SSDYKINNKGASGALNPPYGTI 405
Db 358 TSTRRAITVLGSSAKITNLRAAQOSIFYDYDPLASNTTGSADVLTITNOPDSNPLDIYGTTI 417
OY 406 LFSGFTLTADBLKVADNLKSSFTPOPVLSGGKILLQKQVTLSESTPSQEAAGSLIGMDSGT 465
Db 418 VFSGKTLADEAKADNFTSILKQPLALASGTLALKGNVELDVNGFQTQEGSTLLMQPGT 477
OY 466 TLSTTAGSITITNLGINDSLGLKOPVSLTAIGASKKIVYSGKTLNLDIEGNTYESHMFPS 525
Db 478 KIKADTEAITSLTKLVVDLSALEGNKSVSIETAGANTTITLTSPLVPQDSSGNFESHHTI- 536
OY 526 HDQLESL-LKITVDADVDTNVDISSLIPVAEPDPNSEYFQOGOMNVMTTDTAINTFEAT 584
Db 537 -NQATQGLVVLVTAATAASDIYIDALLTSPVQTPREHYGQGMBAETW-ADTST-AASGT 593
OY 585 ATWTKTGVVSPERKSALVCNTLKGVTFTDRIQLQDLVEIGATGMEHKQGFVWSSMTNPLH 644
Db 594 MTWVTYTNPNPDERBASVVPDLSIMASFTDIRTLOQIMTSQANSIYOORGIMASTAIFPH 653
OY 645 KTGDENRKQFRTSGGYVIGGSANHPKDDLFFFAFCHLFARDDCFIAHNSRTYVGGTLF 704
Db 654 KDKSGTNOAFRHKISGYIVGSSADBPSENIFFSAVAFQULGCKDXDLFVEMTSHNYLASLV 713
OY 705 FKHSHTTOPONYLRGLRAKFSSSAIEKPREIPLADVVSFESHSDNRMETHYTSLPDESE 764
Db 714 LQHRFAFLG-----GLPMPFSGSIITMDLKDIPLLINAAQTSYSTKXMDMTRRYSYBEAQ 766
OY 765 GSWNSHECICLAGLGLDLPVLSNPHPLFKFTIQMKEMVYVSGNSPFESSDDGCFEIGR 824
Db 767 GSWTNNSGALEIGGSLALYLPKEAPPQGYFPFLKQAYVSRQONFESGAEAEAPFDGD 826
OY 825 LNLNTSIPVGAKFVQCDIGDPSYTYDLSGFVSDVYRRNNPOSTALVMSPDMSKIRGKULSR 884
Db 827 LVNGCIPYGIRLEKISIDBKONNFEISLAIYIGDYRRKNPISRSTLWVSGAWTSLCKNULAR 886
OY 885 QAFILRGSNVYVYNSNCELFPHYAMELRRGSSKNRYNVDVGTKLRF 928
Db 887 QAFILASAGSHLTLSPHVELSGEAAVELRGSAAHIVYVDCGLRYSF 930

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RESULT 11
C72078
polymorphic outer membrane protein g family - Chlamydophila pneumoniae (strain CWL029)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: C72078
C:Kaitman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: C72078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-936 <ARN>
A:Cross-references: UNIPROT:Q9Z898; UNIPARC:UPI00000470BC; GB:AE001627; GB:AE001363; NID
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: pmp_7
C:Superfamily: Chlamydophila pneumoniae polymorphic outer membrane protein G

Query Match      36.3%; Score 1734; DB 2; Length 936;
Best Local Similarity 39.9%; Pred. No. 7, 2e-90;
Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

0y      1  MKTSLPWLVSASVLAFCSCLOSLANBELSLPDDSFNGNIDSGF-----TPKTSATYSL 55

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Db 1 MKSSVSWLFFSSLPFLFSSLSIYVAEVTLLDSSNNSYDGS-NGTTFVFTSTDDAAAGTTYSL 59  
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Db 60 LSDVSFQNGALGIFPLASGCFLEAGGDLTFQGNQHALKFAFINAGSAGTAVASTADKN 119  
Qy 114 LTFSGFSLSPDSSPSTTVT-TGQGLTSSAGVNLLENIRKLVVAGNFTSDGGAIKGASF 172  
Db 120 LTFNDFSRLLSIFSGPILLSPTGQCALKSYGNLSLTGNSQIIFQNFSSDNGVINTKNF 179  
Qy 173 LLTGSGDALFSNNSSST--KGGAIAATTAGARIANNNGYVRFSLNISTSGAIDDEGTS 230  
Db 180 LLSGTSQFASFSRNQAFGTGQGVVATGTTTENSQIVSFSQNLAKSGGALYSTDNC 239  
Qy 231 ILSNNKFLYFEGN---AAKTGGAICNTKASGSPELLISNNKTLIPASVNAETSGAIIH 286  
Db 240 SITDNFOVIFDGNASAMEAQAQGAICCTTTDKT--VTLGNKSLSTNNLTALTYGAIS 297  
Qy 287 AKKLALSGGFTFELRNNSATP---KGGAISIDAGELSLSAETGNTTFVNTLTG 343  
Db 298 GLKVISIAGGPTLF-QSNISGSSAGGGGAINIASGELALSATSGDITF-NNNQVTNG 355  
Qy 344 STDTPKRNAINISNGKFTFLRAAKNHTIFFYDPTSEGT--SSDVUKINNGSAGALNPY 401  
Db 356 STST--RNAINIIDTAKVTSIRAAATGOSIFYYDITPAGTAASDTLNLMLADANSIEY 413  
Qy 402 QGTLFSGEITLTADELKVDNLKSFQPVLSGGKLLQKVLTLESTFSQEAAGSLGM 461  
Db 414 GGAIVFSGEKLSPEKAIANAVSTIRQPAVLARGDLVLRGVVTRKDLTQSGSLIM 473  
Qy 462 DSGTTLSTTASITITNLGINVDSLQKQPVSLTAKGASNKVIVSGKLNIDIEGNIYES 521  
Db 474 DGGTTLTSAKEANLSLNGLAIVLSLDGTNKAALKTEADKNISLSGTIALIDTEGSEYEN 533  
Qy 522 HMFHSDQLFSLKLTVDADVNDVNDISLIPVPAEDPNSSEYFGQGNVNMVTTDTANTK 581  
Db 534 HNLKASATYPLLELT-AGANGITTLGALSTLLQEBETHYQGNQWLSMA--NATSSK 590  
Qy 582 EATATWTKGVFVSPERKSALVCTNLWGVTDFDIRSLQOLVEIGATGMEHKQGFVWSMTN 641  
Db 591 IGSINMTRTGYIIPSPERKSNPLNSLMGNFIDIRSIQIIPLESFPAKFSYLTDDHMKTYTDDN 769  
Qy 642 FLHKTGDNKGRFRRHSGVIGVIGSAHTPKDLETFACHLFARDKOCFIAHNNSTYGG 701  
Db 651 FFYRDSMPTRHGRHISGVALGITATTPAEDQLTFACQLFARDRNHITGKNHDTYGA 710  
Qy 702 TLFKHSHTL-QPQNYLRLGAKSESALIEKPREIPLADVOVVSFSDNRMTHTSL 760  
Db 711 SLVPHHTEGFLDIANFL-WGKATRAPVWLSISQIIPLESFPAKFSYLTDDHMKTYTDDN 769  
Qy 761 PESGWSNNECIAGIGLDLPVLSNPHLPFKTFIPQMKVEMVYVVSQNSFFESSSDGRGF 820  
Db 770 SIIRGSRNDAPCADLGASLFPVIVSVY-LKKEVPEPVKQVYIYAHQODFYERAAEGRAF 828  
Qy 821 SIGRLNLSIPVGAKFVQGDIGDSTYYDLSGFVSDVYRNNPOSTATLWMSPDWKIRGG 880  
Db 829 NKSELINEIPIGVTFERDSKSEKTYDILMTYILDAVRNPKCQTSIIASDANMMAYGT 888  
Qy 881 NLSQAFLRGSNNVYVNSCELFGHYAMELRGSSRRNVNVGTRKLP 928  
Db 889 NLAQGFVVRANHPQVNPHEIFQGFQFAFEVRSRRNNTNLGSKPCP 936

## RESULT 12

881581 polymorphic membrane protein G family CP0308 [imported] - Chlamydomonas pneumoniae (stra  
C/Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: B81591  
R/Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A>Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935  
A:Accession: B81591  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-936 <REA>  
A/Cross-references: UNIPROT:Q92898, UNIPARC:UPI0000131CED, GB:AE002193, GB:AE002161, NID:  
A/Experimental source: strain AR39, HL cells  
C/Genetics:  
C:Gene: CP0308  
C:Superfamily: Chlamydomonas pneumoniae polymorphic outer membrane protein G

Query Match 36.2%; Score 1733; DB 2; Length 936;

Best Local Similarity 39.9%; Pred. No. 8.2e-90; Mismatches 356; Indels 32; Gaps 18;

Matches 378; Conservative 182;

Qy 1 MKTISPMVWVSVYLAFCCHLQIANEELSPDSSFGNIDSGT-----TPKTSATYGL 55  
Db 1 MKSSVSWLFFSSLPFLFSSLSIYVAEVTLLDSSNNSYDGS-NGTTFVFTSTDDAAAGTTYSL 59  
Qy 56 TGDFVFEYBPK-GTPUSDSCFKQTTDNLFLNGHSLTFPGIDAGTHAGAASTT-ANKN 113  
Db 60 LSDVSFQNGALGIFPLASGCFLEAGGDLTFQGNQHALKFAFINAGSAGTAVASTADKN 119  
Qy 114 LTFSGFSLSPDSSPSTTVT-TGQGLTSSAGVNLLENIRKLVVAGNFTSDGGAIKGASF 172  
Db 120 LTFNDFSRLLSIFSGPILLSPTGQCALKSYGNLSLTGNSQIIFQNFSSDNGVINTKNF 179  
Qy 173 LLTGSGDALFSNNSSST--KGGAIAATTAGARIANNNGYVRFSLNISTSGAIDDEGTS 230  
Db 180 LLSGTSQFASFSRNQAFGTGQGVVATGTTTENSQIVSFSQNLAKSGGALYSTDNC 239  
Qy 231 ILSNNKFLYFEGN---AAKTGGAICNTKASGSPELLISNNKTLIPASVNAETSGAIIH 286  
Db 240 SITDNFOVIFDGNASAMEAQAQGAICCTTTDKT--VTLGNKSLSTNNLTALTYGAIS 297  
Qy 287 AKKLALSGGFTFELRNNSATP---KGGAISIDAGELSLSAETGNTTFVNTLTG 343  
Db 298 GLKVISIAGGPTLF-QSNISGSSAGGGGAINIASGELALSATSGDITF-NNNQVTNG 355  
Qy 344 STDTPKRNAINISNGKFTFLRAAKNHTIFFYDPTSEGT--SSDVUKINNGSAGALNPY 401  
Db 356 STST--RNAINIIDTAKVTSIRAAATGOSIFYYDITPAGTAASDTLNLMLADANSIEY 413  
Qy 402 QGTLFSGEITLTADELKVDNLKSFQPVLSGGKLLQKVLTLESTFSQEAAGSLGM 461  
Db 414 GGAIVFSGEKLSPEKAIANAVSTIRQPAVLARGDLVLRGVVTRKDLTQSGSLIM 473  
Qy 462 DSGTTLSTTASITITNLGINVDSLQKQPVSLTAKGASNKVIVSGKLNIDIEGNIYES 521  
Db 474 DGGTTLTSAKEANLSLNGLAIVLSLDGTNKAALKTEADKNISLSGTIALIDTEGSEYEN 533  
Qy 522 HMFHSDQLFSLKLTVDADVNDVNDISLIPVPAEDPNSSEYFGQGNVNMVTTDTANTK 581  
Db 534 HNLKASATYPLLELT-AGANGITTLGALSTLLQEBETHYQGNQWLSMA--NATSSK 590  
Qy 582 EATATWTKGVFVSPERKSALVCTNLWGVTDFDIRSLQOLVEIGATGMEHKQGFVWSMTN 641  
Db 591 IGSINMTRTGYIIPSPERKSNPLNSLMGNFIDIRSIQIIPLESFPAKFSYLTDDHMKTYTDDN 769  
Qy 642 FLHKTGDNKGRFRRHSGVIGVIGSAHTPKDLETFACHLFARDKOCFIAHNNSTYGG 701  
Db 651 FFYRDSMPTRHGRHISGVALGITATTPAEDQLTFACQLFARDRNHITGKNHDTYGA 710  
Qy 702 TLFKHSHTL-QPQNYLRLGAKSESALIEKPREIPLADVOVVSFSDNRMTHTSL 760  
Db 711 SLVPHHTEGFLDIANFL-WGKATRAPVWLSISQIIPLESFPAKFSYLTDDHMKTYTDDN 769  
Qy 761 PESGWSNNECIAGIGLDLPVLSNPHLPFKTFIPQMKVEMVYVVSQNSFFESSSDGRGF 820  
Db 770 SIIRGSRNDAPCADLGASLFPVIVSVY-LKKEVPEPVKQVYIYAHQODFYERAAEGRAF 828  
Qy 821 SIGRLNLSIPVGAKFVQGDIGDSTYYDLSGFVSDVYRNNPOSTATLWMSPDWKIRGG 880  
Db 829 NKSELINEIPIGVTFERDSKSEKTYDILMTYILDAVRNPKCQTSIIASDANMMAYGT 888  
Qy 881 NLSQAFLRGSNNVYVNSCELFGHYAMELRGSSRRNVNVGTRKLP 928  
Db 889 NLAQGFVVRANHPQVNPHEIFQGFQFAFEVRSRRNNTNLGSKPCP 936

Db 829 NKSLEINVEIPICVTERDSKSEKGYDLTLMTYLIDAYRRNPCKQISLIASDANMAYGT 888

Qy 881 NLSROAFLLRGSNVYVNSNCELFGHYAMELRGSSRNRYNDVGTCLRF 928

Db 889 NLSROGFVRAANHFQVNPHEIFGQFAFEVRSSSRNRYNTNLGSKPCF 936

RESULT 13

C86546

polymorphic outer membrane protein G family (imported) - Chlamydia pneumoniae (strain C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: C86546

R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi

Nucleic Acids Res. 28, 2311-2314, 2000

A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A/Reference number: A86491; PMID:20330349; PMID:10871362

A/Accession: C86546

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-936 <STO>

A/Cross-references: UNIPROT:Q9Z898; UNIPARC:UP10000131CED; GB:BA000008; NID:g8978817; P1

A/Experimental source: strain J138

C/Genetics:

A/Gene: pmp\_7

C/Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 36.2%; Score 1733; DB 2; Length 936;

Best Local Similarity 39.9%; Pred. No. 8.2e-90;

Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

Qy 1 MKTSIPVAVSVYAFSCCHLOSLANEELSPDPSFNINDSGTF-----TPKTSATYSL 55

Db 1 MKSSVSLFFSSSLPFLPESLSIVAEEVTLDSNNSYDGS-NGTTFVSTTDAAAGTYSL 59

Qy 56 TGDVFFVEPKG-STPLSDSCFKQTTDNLFLNGHSLTFPGIDAGTHAGAASTT-ANKN 113

Db 60 LSDVVFQNALGILPIPLASGCFLEKGDLTFOGQHALKFAFINAGSSAGTASTADKN 119

Qy 114 LTFSSGELLSPDSSPTTVV-TGQGLSSAGVNLKLVVAGNSTDGAIKGASG 172

Db 120 LTFNDFSRSLIICPSSLISPTGQCALKSVGNLSLTGNSOILFTQNSNSGAVINTKNF 179

Qy 173 LITGTSGLDALFSNNSST--KGAIAATTAGARIANTGVYRFLSNIASTSGAIDDEGTS 230

Db 180 LLSGTSGPASFNSQATGKGQGVVATGTTIENSGLVSPQNLAKSGCALYSTDNC 239

Qy 231 ILSNNKFLYEGN---AAKTGALCNTKASGSPILLISNNKTLIFASVNAETSGAIIH 286

Db 240 SITDNFQVIFDGNAMBAQAQGAICCTTTDKT--VTLTGKMLSPNTNTALTYGAIS 297

Qy 287 AKKLALSSGFTFLRNVSATP--KGAISIDASGELSLAFTGNITFVKNLTITTTG 343

Db 298 GLVYSISAGPTLF-OSNIGSSAGGCGGAINASGELSLATSQDITF--NNQVYTG 355

Qy 344 STDPKNAINIGSNGFTELRKAKHTTFYDPTSEG--SSDVKINNGSAGALNPY 401

Db 356 STST--RNAINIITDAKVTISRAATGOSITFYDPTINPRASTDLNMLADANSLEY 413

Qy 402 QGTLIFSGETTLADELKVADNKLSSFTQVYSLSGKLLLOKGYLLESTFSQEAGSLGM 461

Db 414 GGAIVFSGELSPTEKAIANVSTINQPAVLARGDLVLRDGVTVPRKDLTQSGSLIM 473

Qy 462 DSGTTLSTAGSITITNLGINVDSLGKQVSLTAKASKNVIVSGKLNIDIEGNLYES 521

Db 474 DGGTTLISAKRANSLINLAIVNLSDGTNKALKTEAADKNISLSTGIALIDEGSYEN 533

Qy 522 HMFSDQLFSLKTTVDADVDTNVDISLIIPVPAEDNSEYFGQGNVNMVTTDTATNK 581

Db 534 HNLKSAFTPLLETT-AGANGTITLGLSTLIGEBETHYGOGNQLSMA--NATSSK 590

Qy 582 EATATWTKTFVPSPEKSAIVCNTLGVFTDIRSLQOLVEIGATGNEHKGFVSSMTN 641

Db 591 IGSINMTKGTGYPSPERKSNLPLNSIMGNFIDIRSLNQLIETKSGCEPERELIMLSGIN 650

Qy 642 FLHKTDENRKGFRHRSGGVYIGSANTPKDDLTFEPAFCHLPARDXCFIAHNSRTYGG 701

Db 651 FFYRDSMPFRHGRHISGGYALGRTATTPABDQLTFAFCQLPARDNHLTGKHGTYGA 710

Qy 702 TLEFKSHTL-OPNYLRLGRAKFSESAIEKPREIPLALDVQVPSHSDNRMEHTYSL 760

Db 711 SLYFHHTEGLFDIAPNL-MGKATRAPVWVSEISQILPLSFDAKFSYLAHTDNHKKTYTDN 769

Qy 761 PSESGWSNECIAAGIGLDLPVLSNPHLFTFTIPQKVMWVYVYVNSGSESSDGRGF 820

Db 770 SLIKGSWRDAPCADGASLPVIVSYV-LKEVEFPVQYIVAHQODFYERYAEGRAF 828

Qy 821 SIGRLNLSPYGAKEFVQGDIDGSYYDLSGCFPSVYNNQSTATLVMSPDWKRIGG 880

Db 829 NKSLEINVEIPICVTERDSKSEKGYDLTLMTYLIDAYRRNPCKQISLIASDANMAYGT 888

Qy 881 NLSROAFLLRGSNVYVNSNCELFGHYAMELRGSSRNRYNDVGTCLRF 928

Db 889 NLSROGFVRAANHFQVNPHEIFGQFAFEVRSSSRNRYNTNLGSKPCF 936

RESULT 14

H86492

pmp\_3 (imported) - Chlamydia pneumoniae (strain J138)

C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C/Accession: H86492

R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi

Nucleic Acids Res. 28, 2311-2314, 2000

A/Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A/Reference number: A86491; PMID:20330349; PMID:10871362

A/Accession: H86492

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-772 <STO>

A/Cross-references: UNIPROT:Q9RB71; UNIPARC:UP100000CCC33; GB:BA000008; NID:g8978389; P11

A/Experimental source: strain J138

C/Genetics:

A/Gene: pmp\_3\_2

Query Match 33.3%; Score 1591; DB 2; Length 772;

Best Local Similarity 42.7%; Pred. No. 6.1e-82;

Matches 337; Conservative 146; Mismatches 275; Indels 32; Gaps 14;

Qy 153 LVVAGNFTADGAIKGAFLITGSGDALFNSNNSSTGGAIAATTAGARIANTGVYRF 212

Db 1 MFLSKNFTDNGAIIAKTLISLTGTMALFSENTSSKKGAIQTSDALITGNGEVSF 60

Qy 213 LSNIASTSGAIDDEGTSILSNKKFLYF-----EGNAKTT-----GGAICNTKASGSPEL 263

Db 61 SDTSSDSGAALFTEASVTISNNAKVSFIDNKVTGSSSTIGDMSGAICAYKTSIDTVK 120

Qy 264 IISNNKTLIFASVNAETSGAIIHAKKLALSSGFTFLRNVSATP-PKGAISIDASG 322

Db 121 TLTGQMLFNSNNTSTTAGAIYVKLELASGLTIFSNNSVNGCPAPGGAIAIDSG 180

Qy 323 LSLAETGNITVRNLTITGSDTPKRNAINIGSNGKTELRKAKNHTTFYDPTT--S 380

Db 181 LSLASDSGDIVFGNTVST--TPGTRRSSIDLGSARKMTALRSAGRAIYFPDPTTGS 238

Qy 381 EGTSSDVLRKINNGSAGALNPYOGTILFSGETTLADELKVADNKLSSFTQVYSLSGKLL 440

Db 239 STTVTVLVKNETPADSALQYTGNIIFTEKLSFTBAOSKULTSLDLPVTLISGGLSL 298

Qy 441 QKGVTLSETSFSQAGSLGMDGTTLTSTAAGITITNLGINVDSLGKQVSLTAKGAS 500

Db 299 KIGCVTLQTAFAFQOADSRLMDVGTLE-PADSTINNLVINISSIDGAKKAIETKATS 357

Qy 501 NKVIYSGKLNIDIEBNITESHMFSDQLPSLKITVADVDTNVDISLIIPVPAEDPNS 560

Db 358 KMLTISGTTLLDPGTGFYENHSLRNPQSYDILEKASGTVS---TAVTPDPIWGEKF 413

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Qy 561 EYEGQOQM-VNWTTPDATNKEATATMTKGFVPSBERKSALVONTLMGTFDIRBLOQ 619
Db 414 HYGQGTWGPJLWVGASTT---ATFWMTKGYLPNBRIGSLVBNLMAFIDISLHY 470
Qy 620 LVEIGATGMEHKQGFVWSMTNPLFKTGTDEBRKQFRRHTSGGYVIGSAAHTPKDLPFAF 679
Db 471 LMEFANEGLOQDRAFWCAGLSNFPHKOSTTKRRGFRHSSGYVIGSNLHTCSKDLISAAF 530
Qy 680 CHLFARDCEFIANNHSTYGTLLFPKSHTLQDONYLRLGRAKFSSEALIEKPREIPLA 739
Db 531 CQLFRDRDYPVAKNQGTVGTLYGHNEL-----YLSL-PCKLRCSLSYVTEIPVL 584
Qy 740 LDVOVSSHSHNNRMEHTYLSLPSBEGSKNSNCIAGIGLDLPVLVSNPHLPFKTFIQMK 799
Db 585 FSGNLSYHTNDNDIKXTYTPYVKGSGWGNDSFALFEGRAPICL-DESALEQYMPFMK 643
Qy 800 VEMTYVSONSPFESSSDGRGFSIGRLNLSLIPVCAKF-VQGDIDSYTYDLSGFSVDY 858
Db 644 LQFYVAHQEGKEQGTENRFGSSRLVNLAPIGRPFKESDCDA-TYNTLTGITYDVLV 702
Qy 859 RNNPOSTATLVMSDPDWIKRIGNLSRQAFLLRGSNNVYVNSNCELFQHYAMELRGSSRNY 918
Db 703 RSNPDCTTTLISGDSWMTFCGTLNARQALVLRAGNHFCFNSNFEAFSQFSFELRGSSRNY 762
Qy 919 NVDVGTKLRF 928
Db 763 NVDLGAKYOF 772

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RESULT 15
E72130 polymorphic membrane protein G family CP0761 [imported] - Chlamydia pneumoniae (strain
C:Species: Chlamydia pneumoniae pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: E72130; G81541
R:Kaitman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72130
A:Molecule type: DNA
A:Residues: 1-841 <ARN>
A:Cross-references: UNIPROT:Q9Z3A1; UNIPARC:UPI00000470B5; GB:AE001586; GB:AE001363; NIDN
A:Experimental source: strain CHL029
R:Reed, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: G81541
A:Molecule type: DNA
A:Residues: 1-841 <RNA>
A:Cross-references: UNIPARC:UPI00000470B5; GB:AE002235; GB:AE002161; NID:G7189672; PIDN
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: pmp 2; CP0761
A:Superfamily: Chlamydia pneumoniae pneumoniae polymorphic outer membrane protein G

Query Match 30.0%; Score 1435.5; DB 2; Length 841;
Best Local Similarity 35.9%; Pred. No. 4e-79;
Matches 340; Conservative 147; Mismatches 335; Indels 125; Gaps 15;

QY 1 MKTSLPWLVSVLAFS-CHLOSLANFELSLDDSPFNINDSGFTPTKTS----TTSLS 55
DB 1 MKIPFLPLISLVPLTSLNSNLGAATTEBLASANSFDDGTSTTSSSKTSKTSYDGTNYVF 60
QY 56 TGDVFFVE-PGKGTPLSDSCFKQ--TTDNLTFPLGHSITFGFDIAGTHAGA--ASTTAN 111
DB 61 KDSVVIENVPKGTGERQSTSCFNDAAGDLNLFGGGFSFTFENIDATTASGAALGSEAN 120
QY 112 KNLTFSSGSLSLFSDSPSTTTVTTGGGTLSAGGVNLENIKRLVVGANSTADGAIKAS 171

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|    |     |   |     |
|----|-----|---|-----|
| Db | 121 | KTVTLSGFSALSPKSPASTVTVNGLGAINVKNLSLDNDKVLIQDNFSTDDGAINCAG     | 180 |
| Qy | 172 | FLTGTSGDALFSNNSSSTKGAIAATTAGARIANNVTGYVELSNIASTSGAIDDEGTSI    | 231 |
| Db | 181 | -----   | 180 |
| Qy | 232 | LSNNKFLYFEGNAAKTTGGALCNTKASGPPELLISNNKTLIPASVNAETSGAIHAKULA   | 291 |
| Db | 181 | -----SLKIANNKSLAFIGNSSSTRGAIHTTKMLT                           | 210 |
| Qy | 292 | LSSGGFPEFLANNVSATPKGGAISIDASGSLSLAEFGNTTFVKNLTITTTGSDTPKRN    | 351 |
| Db | 211 | LSSGGFTLFOGNTPTPAAGKGAIAIADSGTSLISIGSDGIIIFRENTI--GAGTGVSHS   | 267 |
| Qy | 352 | AINGSNKFEFLAAKNHTFEFDPTSECTSS--DVLKTNNGSAGALNPOGTLPSG         | 409 |
| Db | 268 | AIDGTSKATLALPAOQHTIYFPDPTVTGSTADALNINSPDTGNKKEYTGIIVSG        | 327 |
| Qy | 410 | ETLVADELKAVDNKKSFTQPVSLISGGKLLLOKGVTLESTFSQEGSLLGMDSGTTPST    | 469 |
| Db | 328 | EKLTEAEKDEKKNKTSKLLQNVAPKNGTVVLKGDVLSANFSGQDANSKLLMDGTSILVA   | 387 |
| Qy | 470 | TAGSITTNLGINVDSLGLKQPVSLTAKGANSKYVSGKMLIDIEGNIYESHMFSDQL      | 529 |
| Db | 388 | NTESELNLNLINIDSLNGKKIKLSAATAQKDIRIDRPVLAIASDESFYQNGFLNEDHS    | 447 |
| Qy | 530 | F-SLIKTITVDADVDTNVDISLIPYPAEDPNSEFGQGMNVNNTTDPATNTKEATATWT    | 588 |
| Db | 448 | YDGIJELDAGKDIIYIASDNRSIDAV-----OSPXYOQKWTINMSTD---DKKATVSWA   | 498 |
| Qy | 589 | KTFGVPSPERSALVVCNTLKGVPFNDIRSLQOLVELGATGMHKGQFWVSMNTEPLHKTD   | 648 |
| Db | 499 | KQSFPTLAEQAPLVPNLLMGSFIDVRSFQNTIELTGAPAEKKEFWAGISNVVLRSGR     | 558 |
| Qy | 649 | ENRKGFRTSGGYVIGSAGTAPKODLPFAFCHLPARDKCEFIANNSTRYTGTLFFKHS     | 708 |
| Db | 559 | ENOKFRHVSAGAVVAGASTRMPGDDTSLGPAQLFAPKDYFPMNTNPAKTAIGASLRLOHD  | 618 |
| Qy | 709 | HTLPONYLRLGRAKFSESAIEKPREIPLALDVQVSFSDNRMETHYTSIP-----        | 761 |
| Db | 619 | ASLVSVSVILLEGSLREIILPVPYSKTLPCSEYQGLSTGHDHMKTE--SLPPPTPLS     | 676 |
| Qy | 762 | ESGGSWSNECTIAGIGIDLFPVLNSPHDLPTFTLIPOMKVENYVYVSQNSFFESSDGRGHS | 821 |
| Db | 677 | TDHNSWGYVWAAGELGTRVAVENTSGRFPQGYTBFVQAVYARQDSFVELGAIASRDFS    | 736 |
| Qy | 822 | IGRLINLSIPYGAKVQGDIGDSTYYDLSGFFVSQVYRNNPOSTATLVMSPPSKILRGDN   | 881 |
| Db | 737 | DSHLVNLAIPLGIK-LEKRFABQY-YHVAVMVSPPVCSRNPCKTITLLSNOGSMYTKGSN  | 794 |
| Qy | 882 | LSRQAFLLRGSNNYYNNSNCELFHYAMELGSSNNVNVVDGCTKRF                 | 928 |
| Db | 795 | LARQAGIVQASGFRSLGAALFNGFGEWKGSSSAYVNDASKIKF                   | 841 |

Search completed: November 25, 2005, 14:21:16  
Job time : 28.1039 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2005, 13:58:10 ; Search time 141.033 seconds  
(without alignments)  
4642.376 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 4782  
Sequence: 1 MKTSIPWLVSSVLAFSCHL.....MELRGSSRYNYDVGTKLRF 928

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1          | 4782   | 100.0       | 928    | 1     | PMPL1_CHLPP |
| 2          | 1882   | 39.4        | 942    | 1     | PMPL1_CHLPP |
| 3          | 1802   | 37.7        | 926    | 2     | PMPL1_CHLPP |
| 4          | 1802   | 37.7        | 926    | 2     | PMPL1_CHLPP |
| 5          | 1794   | 37.5        | 926    | 1     | PMPL1_CHLPP |
| 6          | 1791   | 37.5        | 926    | 1     | PMPL1_CHLPP |
| 7          | 1785   | 37.3        | 928    | 1     | PMPL1_CHLPP |
| 8          | 1761   | 36.8        | 930    | 1     | PMPL1_CHLPP |
| 9          | 1733   | 36.2        | 936    | 1     | PMPL1_CHLPP |
| 10         | 1598   | 33.4        | 866    | 2     | PMPL1_CHLPP |
| 11         | 1591   | 33.3        | 772    | 2     | PMPL1_CHLPP |
| 12         | 1562.5 | 32.7        | 839    | 2     | PMPL1_CHLPP |
| 13         | 1546.5 | 32.3        | 841    | 2     | PMPL1_CHLPP |
| 14         | 1535   | 32.1        | 846    | 2     | PMPL1_CHLPP |
| 15         | 1532.5 | 32.0        | 847    | 2     | PMPL1_CHLPP |
| 16         | 1435.5 | 30.0        | 841    | 1     | PMPL1_CHLPP |
| 17         | 1353   | 28.3        | 922    | 1     | PMPL1_CHLPP |
| 18         | 1284.5 | 26.9        | 973    | 1     | PMPL1_CHLPP |
| 19         | 1282   | 26.8        | 1024   | 2     | PMPL1_CHLPP |
| 20         | 1275   | 26.7        | 1378   | 2     | PMPL1_CHLPP |
| 21         | 1259.5 | 26.3        | 1011   | 2     | PMPL1_CHLPP |
| 22         | 1237.5 | 25.9        | 843    | 2     | PMPL1_CHLPP |
| 23         | 1222   | 25.6        | 700    | 2     | PMPL1_CHLPP |
| 24         | 1205   | 25.2        | 1276   | 1     | PMPL1_CHLPP |
| 25         | 1203   | 25.1        | 1276   | 1     | PMPL1_CHLPP |
| 26         | 1198   | 24.8        | 602    | 2     | PMPL1_CHLPP |
| 27         | 1188   | 24.7        | 601    | 2     | PMPL1_CHLPP |
| 28         | 1183.5 | 24.1        | 843    | 2     | PMPL1_CHLPP |
| 29         | 1153.5 | 23.5        | 591    | 2     | PMPL1_CHLPP |
| 30         | 1125.5 | 23.1        | 581    | 2     | PMPL1_CHLPP |
| 31         | 1105.5 | 23.1        | 581    | 2     | PMPL1_CHLPP |

#### ALIGNMENTS

| RESULT 1 | PMPL1_CHLPP  | STANDARD | PRT | 928 AA |
|----------|--|----------|-----|--------|
| AC       | 086164   | Q9K299   |     |        |
| DT       | 16-OCT-2001 (Rel. 40, Created)   |          |     |        |
| DT       | 16-OCT-2001 (Rel. 40, Last sequence update)  |          |     |        |
| DT       | 10-MAY-2005 (Rel. 47, Last annotation update)  |          |     |        |
| DE       | Probable outer membrane protein pmpl1 precursor (Polymorphic membrane protein 11) (Outer membrane protein 4)       |          |     |        |
| GN       | Name=pmpl1; Synonyms=omp4; OrderedlocusNames=CP00449, CP0002, CPB0468;   |          |     |        |
| OS       | Chlamydia pneumoniae (Chlamydia pneumoniae)  |          |     |        |
| OC       | Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia   |          |     |        |
| OX       | NCBI_TaxID=83558;  |          |     |        |
| RN       | [1]  |          |     |        |
| RP       | NUCLEOTIDE SEQUENCE  |          |     |        |
| RC       | STRAIN=CWLO29/VR-1310;   |          |     |        |
| RX       | MEDLINE=20007584; PubMed=9864239;  |          |     |        |
| RA       | Krudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;   |          |     |        |
| RT       | "Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae"; |          |     |        |
| RL       | Infect. Immun. 67:375-383(1999).   |          |     |        |
| RN       | [2]  |          |     |        |
| RP       | NUCLEOTIDE SEQUENCE  |          |     |        |
| RC       | STRAIN=CWLO29 / VR1310;  |          |     |        |
| RX       | MEDLINE=99206606; PubMed=10539856;   |          |     |        |
| RA       | Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,   |          |     |        |
| RT       | "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity";                |          |     |        |
| RL       | Am. Heart J. 138:5491-5495(1999).  |          |     |        |
| RN       | [3]  |          |     |        |
| RP       | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]  |          |     |        |
| RC       | STRAIN=CWLO29;   |          |     |        |
| RX       | MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716;   |          |     |        |
| RA       | Kalman S., Mitchell W.P., Marathe R., Lamme C.J., Fan J., Hyman R.W.,  |          |     |        |
| RT       | Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  |          |     |        |
| RL       | "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";  |          |     |        |
| RN       | Nat. Genet. 21:385-389(1999).  |          |     |        |
| RP       | [4]  |          |     |        |
| RC       | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]  |          |     |        |
| RX       | MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;  |          |     |        |
| RA       | Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,   |          |     |        |
| RT       | White O., Hickey E.K., Peterson J.D., Uterback T.R., Berry K.J.,   |          |     |        |
| RL       | Bass S., Linher K.D., Weidman J.F., Kouri H.M., Craven B., Bowman C.,  |          |     |        |
| RN       | Docson R.J., Grim W.L., Nelson W.C., Deboy R.T., Kolonay J.F.,   |          |     |        |
| RA       | McCarty G., Salzberg S.L., Eisen J.A., Frazer C.W.;  |          |     |        |
| RT       | "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39";                                    |          |     |        |
| RL       | Nucleic Acids Res. 28:1397-1406(2000).   |          |     |        |
| RN       | [5]  |          |     |        |
| RC       | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]  |          |     |        |
| RX       | STRAIN=Q138;   |          |     |        |
| RA       | MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;   |          |     |        |



RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.,  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
RT from Japan and CML029 from USA."  
RL Nucleic Acids Res. 28:2311-2314(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
RC STRAIN=TW-183;  
RA Geng M.M., Schumacher A., Muehlhofer I., Benesch K.W., Schaefer K.P.,  
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.,  
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with  
RT other Chlamydia strains based on whole genome sequence analysis."  
RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)  
CC (potential).  
CC -1- SIMILARITY: Belongs to the PMP outer membrane protein family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL: AJ001311; CA004672.1; -; Genomic DNA.  
CC EMBL: AJ133034; CAB37072.1; -; Genomic DNA.  
CC EMBL: AE001628; AAD18593.1; -; Genomic DNA.  
CC EMBL: AE002192; AAF38159.1; ALT INIT; Genomic DNA.  
CC EMBL: BA000008; AAA98658.1; -; Genomic DNA.  
CC EMBL: AE017158; BAA98399.1; -; Genomic DNA.  
CC PIR: D72077; D72077.  
CC PIR: H86546; H86546.  
CC PHCI-2DPAGE; O86164; -.  
CC TIGR: CP0302; -.  
CC InterPro: IPR005546; Auto\_transpbeta.  
CC InterPro: IPR011427; ChlamPMP\_M.  
CC InterPro: IPR003368; Chlamydia\_PMP.  
CC Pfam: PF03797; Autotransporter; 1.  
CC Pfam: PF02415; Chlam\_PMP; 6.  
CC Pfam: PF07548; ChlamPMP\_M; 1.  
CC TIGRFPMS: TIGR01376; POMP\_repeat; 5.  
CC Complete proteome; Membrane; Multigene family; Outer membrane; Signal.  
FT SIGNAL  
FT CHAIN  
SQ SEQUENCE 928 AA; 98904 MM; 788BCDD62C911402 CRC64;  
Query March 100.0%; Score 4782; DB 1; Length 928;  
Best local similarity 100.0%; Pred. No. 1.3e-256;  
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKTSIPWLVSSVLAFAFCHLOSLANBELLSPPDSFNGNIDSGTTPKTSATTVSLTGDFV 60  
DB 1 MKTSIPWLVSSVLAFAFCHLOSLANBELLSPPDSFNGNIDSGTTPKTSATTVSLTGDFV 60  
QY 61 FYEPGKGTPLSDSCFKQTTDNLTLFGNGHSLTFGFIADGTHAGAAASTTANKNLTPSGFS 120  
DB 61 FYEPGKGTPLSDSCFKQTTDNLTLFGNGHSLTFGFIADGTHAGAAASTTANKNLTPSGFS 120  
QY 121 LLSDDSSSTVTGGGGLSSAGGNLEIRKLVAGFSTADGAIKGAFFLLTGSGD 180  
DB 121 LLSDDSSSTVTGGGGLSSAGGNLEIRKLVAGFSTADGAIKGAFFLLTGSGD 180  
QY 181 ALFENNSSSTKGAIAATTAGARIANNITYRFLSNIASTSGAIDDEGTSILSNKKFLYF 240  
DB 181 ALFENNSSSTKGAIAATTAGARIANNITYRFLSNIASTSGAIDDEGTSILSNKKFLYF 240  
QY 241 EGNAAKTGGAI CNTKASGSEPLLII SNKTLII PANSVAETSGAIHAKKALSSGGTFEF 300  
DB 241 EGNAAKTGGAI CNTKASGSEPLLII SNKTLII PANSVAETSGAIHAKKALSSGGTFEF 300  
QY 301 LRRNVSSATPKGGAISIDASGELSIAFTGNITFPARNLTTTGSMDTPKRAAINIGSNGK 360  
DB 301 LRRNVSSATPKGGAISIDASGELSIAFTGNITFPARNLTTTGSMDTPKRAAINIGSNGK 360

QY 361 FTFLRAAKNHTTFPYDPITSEGTSSDVLKINNSAALNPYQGTILPSGTTLTADBLKVA 420  
DB 361 FTFLRAAKNHTTFPYDPITSEGTSSDVLKINNSAALNPYQGTILPSGTTLTADBLKVA 420  
QY 421 DNLKSFQPVSLSGGGLLQKGVTLSESTSFSGEASLLGMDGTLSTAGSIITTNLG 480  
DB 421 DNLKSFQPVSLSGGGLLQKGVTLSESTSFSGEASLLGMDGTLSTAGSIITTNLG 480  
QY 481 INVDSGLKQPVSLTAKGASNKIVSGKLNLIIEGNIYESHMFSDQLPSLKITVDAD 540  
DB 481 INVDSGLKQPVSLTAKGASNKIVSGKLNLIIEGNIYESHMFSDQLPSLKITVDAD 540  
QY 541 VDTNVDSISLLIYPADBPNSSEYFGQGMVNNWTTDTATNKAATATWTGTGVPSPBRKS 600  
DB 541 VDTNVDSISLLIYPADBPNSSEYFGQGMVNNWTTDTATNKAATATWTGTGVPSPBRKS 600  
QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWSMTNPLHKTGDENRKGFRTSGG 660  
DB 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWSMTNPLHKTGDENRKGFRTSGG 660  
QY 661 YVIGSAHTPKDGLTFPAFCHLPARDKCFIAHNSRTYGTLPFGHSHTLQPNYLRIG 720  
DB 661 YVIGSAHTPKDGLTFPAFCHLPARDKCFIAHNSRTYGTLPFGHSHTLQPNYLRIG 720  
QY 721 RAKFSESAIEKPREIPLADVVSFSDNRMEHTYSLPESGSMNECIAIGIGDL 780  
DB 721 RAKFSESAIEKPREIPLADVVSFSDNRMEHTYSLPESGSMNECIAIGIGDL 780  
QY 781 PFLSNHPLPKFTIPIQMKEMVYVONSFEESSDGRGSIICRLNLSTIPVAKFVQGD 840  
DB 781 PFLSNHPLPKFTIPIQMKEMVYVONSFEESSDGRGSIICRLNLSTIPVAKFVQGD 840  
QY 841 IGDSTYTDLSGFVSDVYRNNPOSTATLVMSPSWKIRGSLRQAFLLRGSNNVYNSN 900  
DB 841 IGDSTYTDLSGFVSDVYRNNPOSTATLVMSPSWKIRGSLRQAFLLRGSNNVYNSN 900  
QY 901 CELFGHAMELRGSSRRNVVDVGTKLRF 928  
DB 901 CELFGHAMELRGSSRRNVVDVGTKLRF 928  
RESULT 2  
Q823X1.CHLCV PRELIMINARY; PRT; 942 AA.  
ID Q823X1.CHLCV PRELIMINARY; PRT; 942 AA.  
AC Q823X1;  
DT 01-JUN-2003 (TREMblrel. 24, Created)  
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
DE Polymorphic outer membrane protein G family protein/autotransporter,  
DE putative.  
GN OrderedLocustNames=CAA00282;  
OS Bacteriia; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydochilla.  
OC NCI\_TaxID=83357;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=GPIC;  
RC MEDLINE=2256915; PubMed=12682364; DOI=10.1093/nar/31.21.4171;  
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,  
RA Heidelberg J.F., Holtzapfel E.K., Knouri H.M., Fedorova N.B.,  
RA Carty H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.J.,  
RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,  
RA Bavoil P.M., Fraser C.M.;  
RT "Genome sequence of Chlamydochilla caviae (Chlamydia psittaci GPIC):  
RT examining the role of niche-specific genes in the evolution of the  
RT Chlamydiaceae."  
RL Nucleic Acids Res. 31:2134-2147(2003).  
CC EMBL: AE016995; AAP05033.1; -; Genomic DNA.  
CC TIGR: CAA00282; -.  
CC GO: GO:0019967; C:outer membrane; IEA.  
CC InterPro: IPR005546; Auto\_transpbeta.  
CC InterPro: IPR011427; ChlamPMP\_M.  
CC InterPro: IPR003368; Chlamydia\_PMP.





Dh 535 GGIQLSGKGSV-TTTNPSHVGVAE---THYGYQGMSVSWKDNNSDPKTOIAFTWN 590  
Qy 589 KTGFVPSPERKALVCNTLWGVTDIRSLQQLVEIGATG-MEHKQGFVWSMTNPLHKTG 647  
Dh 591 KTGVNPERARAPLVNLSLWGSFIDLSIQDLERSVDSILETRGLWVGIGFFHKDR 650  
Qy 648 D-ENRKGFRTSGGVIGSGAHTPKDILFTFAFCHLPARDKOCFIAHNSRTYGTLPFK 706  
Dh 651 NAEHRK-FRHISSGVIGATNTSREDLSVAFCQFAKDKDYLVSKNAANVAVGASYQQ 709  
Qy 707 HSHTLQPNVNLRLGRKSESIAIEKFPREIPLADLVQVPSFSHSDNRMETHTSLPESEGS 766  
Dh 710 HVSKFDDTLRLPFG---PNTCCSGFSKEIPFLDAQITTYCHTANNMTTSTYDPEVKG 765  
Qy 767 WSNECIAGGIGLDLPF-VLSNPHPLPKFTIPQMKVEMVYVQNSFFESSDGRGFSIGRL 825  
Dh 766 WGNITLGLTLSTVPIPVFSS--SIFDSYAPFAKLVVYAHQDDPKETTEGRTFESSDL 823  
Qy 826 LNLISIPVGAKEVQDIDGSTYTYDLSGFFVSDVYRNPNQSTATLVMSPDMSKIRGNLSRQ 885  
Dh 824 LNVSVPIGIFKEKLSYGERSAVDLTLMYIPVYRHNPSCTGALINDVSWLTATNLARQ 883  
Qy 886 AFLRGSNVYVNSNCELFGHYAMELRGSSRNRYNDVGTCLRF 928  
Dh 884 AFIVRAGNHIALTSGVEMFSQFPELRSSRNRYNDVIGAKVAF 926

## RESULT 4

OSL6J3\_CHLAB PRELIMINARY; PRT; 926 AA.  
ID OSL6J3\_CHLAB  
AC OSL6J3;  
DT 01-FEB-2005 (TRENBLREL. 29, Created)  
DT 01-FEB-2005 (TRENBLREL. 29, Last sequence update)  
DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)  
DE Polymorphic outer membrane protein.  
GN Name=pmp1G; Synonyms=pomp98A; OrderedLocuNames=CAB282;  
OS Chlamydia abortus.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
NCBI\_TaxId=83555;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
RC STRAIN=526/3;  
RX PubMed=15837807; DOI=10.1101/gr.368405;  
RA Thomson N.R., Yeates C., Bell K., Holden M.T.G., Bentley S.D.,  
RA Livingston M., Cerdano-Tarraga A.-M., Harris B., Doggett J.,  
RA Ormond D., Mungall K., Clarke K., Fellwell T., Hance Z., Sanders M.,  
RA Quail M.A., Price C., Barrett B.G., Parkhill J., Longbottom D.;  
RT "The Chlamydia abortus genome sequence reveals an array of  
RT variable proteins that contribute to interspecies variation.";  
RL Genome Res. 15:629-640 (2005).  
DR EMBL; CR848038; CAH63732.1; -; Genomic\_DNA.  
KW Complete proteome.  
SQ SEQUENCE 926 AA; 98440 MW; F81C2A79A3D575D1 CRC64;

Query Match 37.7%; Score 1802; DB 2; Length 926;  
Best Local Similarity 40.8%; Pred. No. 2.5e-91;  
Matches 385; Conservative 172; Mismatches 354; Indels 32; Gaps 15;

Qy 1 MKTSLPWLVNSVLA--FSCHQSLANELLSPDSPFGNIDSGFTPKTATT-----YS 54  
Dh 1 MKPSLYKLISSTLTLPISFHSQJHAEEVALQESILDAN--GAFSPQSTSTAGCTIYN 57  
Qy 55 LTGVDFEPEPGKGTPLSDSCFKQTTDNLTFLNGHSLTFGFIADQTHAGAASTANRL 114  
Dh 58 VESDLSIYDVQGTALASSAFVQTADNLTFLKGNHSLSTTANANRAGINVTADKIL 117  
Qy 115 TFSGSLSPDSSPSTVYTTGGTSLSSAGVNLNIRKLVVAGNFSTADGAIKASFL 174  
Dh 118 TLTDSKLSFKPCPSLVTGKAMKSGALNLANNASILLPQONYSANNGAISCARSL 177  
Qy 175 TGTSGDALFSNNSSSTKGAITTAGARIANTGVVPLSNIASTSGAIDEGSILSN 234  
Dh 178 TGSSKEISFTTNSAKGALAAATGIAHLSDNGTIFRSGNTAVNSGAVVSEASMTIAG 237

Qy 235 NKELYFEGNAKTT---GALCNTRASGSPELLSNKTLIPASVASTSGAIIHAKU 290  
Dh 238 NNVAVSNNAVSSSDGCGGAHCSKTGSAPLTTRIDNKVLIFEENTSSAKGAIYTDKL 297  
Qy 291 ALSSGFTPELRNNVSATPKGAGISIDAGELSLAEFGNITFVNTLTITGSDTTPR 350  
Dh 298 ILTSGPTAIAINKVTHAPPKGAGIAIANGETSLAEHGDTF-DNNLMATQDNATIKR 356  
Qy 351 NAINISNGKFTELRAKKNHTIPFYDPTISEGSSDVLKINNSAGALNPQGTILFSGS 410  
Dh 357 NAINISNGKFTVLRPAASGKTIIFYDPTIVEGAADLTINKAEGD-KTYNRILLFSGE 414  
Qy 411 TLTADELKVAADNLKSSFTQPVSLSGKLLIQKVTLESTFSQAGSLGMDGTLSTT 470  
Dh 415 KLTQEOAAVADNLKTFQPTITLAEGLVRSGEVEAKTVQTAGSLILMDAGTKLSAK 474  
Qy 471 AGSITITNLGINDSLQKQPVSLTAKGANKYVGGKNTLIDIBENIYESHMFHQDLF 530  
Dh 475 TEDATITNLAINENTLDGKKFAVVDAVAAKNVTLSGAIGVLDPTGKFENHRLDPTLAL 534  
Qy 531 SLKIFVDAVDVTVNDISSLIPIVPAEDPNSYGFQCGOMVNMVTTDTATNTEKATA--TWT 588  
Dh 535 GGIQLSGKGSV-TTTNPSHVGVAE---THYGYQMSVSWKDNNSDPKTOIAFTWN 590  
Qy 589 KTGFVPSPERKALVCNTLWGVTDIRSLQQLVEIGATG-MEHKQGFVWSMTNPLHKTG 647  
Dh 591 KTGVNPERARAPLVNLSLWGSFIDLSIQDLERSVDSILETRGLWVGIGFFHKDR 650  
Qy 648 D-ENRKGFRTSGGVIGSGAHTPKDILFTFAFCHLPARDKOCFIAHNSRTYGTLPFK 706  
Dh 651 NAEHRK-FRHISSGVIGATNTSREDLSVAFCQFAKDKDYLVSKNAANVAVGASYQQ 709  
Qy 707 HSHTLQPNVNLRLGRKSESIAIEKFPREIPLADLVQVPSFSHSDNRMETHTSLPESEGS 766  
Dh 710 HVSKFDDTLRLPFG---PNTCCSGFSKEIPFLDAQITTYCHTANNMTTSTYDPEVKG 765  
Qy 767 WSNECIAGGIGLDLPF-VLSNPHPLPKFTIPQMKVEMVYVQNSFFESSDGRGFSIGRL 825  
Dh 766 WGNITLGLTLSTVPIPVFSS--SIFDSYAPFAKLVVYAHQDDPKETTEGRTFESSDL 823  
Qy 826 LNLISIPVGAKEVQDIDGSTYTYDLSGFFVSDVYRNPNQSTATLVMSPDMSKIRGNLSRQ 885  
Dh 824 LNVSVPIGIFKEKLSYGERSAVDLTLMYIPVYRHNPSCTGALINDVSWLTATNLARQ 883  
Qy 886 AFLRGSNVYVNSNCELFGHYAMELRGSSRNRYNDVGTCLRF 928  
Dh 884 AFIVRAGNHIALTSGVEMFSQFPELRSSRNRYNDVIGAKVAF 926

## RESULT 5

PMP9\_CHLPN STANDARD; PRT; 928 AA.  
ID PMP9\_CHLPN  
AC Q92358;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Probable outer membrane protein pmp9 precursor (Polymorphic membrane protein 9) (Outer membrane protein 10).  
GN Name=pmp9; Synonyms=omp10; OrderedLocuNames=Cpn0447, CP0306, CP0464;  
OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
NCBI\_TaxId=83558;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CWI028 / VR3310.  
RX MEDLINE=20007584; PubMed=10539856;  
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,  
RA Madsen A.S., Knudsen K., Falk E., Birke Lund S.;  
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their  
RT role in immunopathogenicity";  
RL Am. Heart J. 138:S491-S495 (1999).  
RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=CWL029;  
RX MEDLINE=9920606; PubMed=10192388; DOI=10.1038/7716;  
RA Kaiman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.,  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";  
RL Nat. Genet. 21:385-389(1999).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=AR39;  
RX MEDLINE=2015025; PubMed=10684935; DOI=10.1093/nar/28.6.1397;  
RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,  
RA Bass S., Lihner K.D., Weisman J.F., Khouri M., Craven B., Bowman C.,  
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,  
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis Morn and Chlamydia  
pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=J138;  
RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi K., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
from Japan and CWL029 from USA.";  
RL Nucleic Acids Res. 28:2311-2314(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=TW-183;  
RA Geng M.W., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,  
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;  
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with  
other Chlamydia strains based on whole genome sequence analysis.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
CC - SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)  
(Potential).  
CC - SIMILARITY: Belongs to the PMP outer membrane protein family.  
CC - SIMILARITY: Contains 1 autotransporter (TC 1.B.12) domain.  
CC -----  
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CC removed.  
CC -----  
DR EMBL; AJ133034; CAB37069.1; -; Genomic DNA.  
DR EMBL; AE001628; AAD18591.1; -; Genomic DNA.  
DR EMBL; AE002192; AAF38163.1; -; Genomic DNA.  
DR EMBL; BA000008; BAA98655.1; -; Genomic DNA.  
DR EMBL; AE017158; AAP98395.1; -; Genomic DNA.  
DR PIR; B72077; B72077.  
DR PIR; E86546; E86546.  
DR TIGR; CP0306; -.  
DR InterPro; IPR005546; Auto\_transp\_beta.  
DR InterPro; IPR006315; Autotransporter.  
DR InterPro; IPR011427; ChlamPMP\_M.  
DR InterPro; IPR003368; Chlamydia\_PMP.  
DR InterPro; IPR006626; Pdh1.  
DR Pfam; PF03797; Autotransporter; 1.  
DR Pfam; PF02415; Chlam PMP; 7.  
DR Pfam; PF07548; ChlamPMP\_M; 1.  
DR SMART; SM00710; Pdh1; 5.  
DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
DR TIGRFAMs; TIGR01376; POMP\_repeat; 6.  
KM Complete proteome; Membrane; Multigene family; Outer membrane; Signal.  
FT SIGNAL 1  
FT CHAIN 26  
FT SEQUENCE 27 928 Probable outer membrane protein pmp9.  
SQ SEQUENCE 928 AA; 9833 MM; 58910A8F04F12219 CRC64;

Query Match 37.5%; Score 1794; DB 1; Length 928;  
Best Local Similarity 42.7%; Pred. No. 6.9e-91;

Matches 404; Conservative 152; Mismatch 353; Indels 38; Gaps 17;  
QY 1 MKTSIMVSVSYLAASCHLQ-----SLANEELSPDSFNGNIDSGTFP-----KTSAT 51  
DB 1 MSSSLMFWLSSLLPLPLNLSAPAAVEINLGFNFSG---PFTYTPPAQTNADET 57  
QY 52 TYSLNGVDFEYBEGKTPIDSCFKQTNDNLFLNGHSLTRGFIDAGTHAGAASTAN 111  
DB 58 IYVLTDVGIITVAGSPITALTASCCKETGNLSFGHGQYFLIONIDAGANC-TFTWTAN 116  
QY 112 KULTFSGFLSFDSSPSTVTYTGCTLSSAGVNLNRIKLVAAGNEFSTAOGALIKGAS 171  
DB 117 KILSFSGFYSLS--LQTNATATGAIKSTGACSTQSNVSCYFGGNFSDNGALAQGS 174  
QY 172 FLITGSGALFSGNNSSTKGAIAATTAGAIANNNGYRPLSNISTSGAIDDEGTSI 231  
DB 175 ISLS-LNPULTRAKKATOKGALYSTGITTINTLNSAFSENTAANGALYTBASSF 233  
QY 232 LSNKPELYEEN---AAKTTGAI-CNTKASGSPELIISNKTLLIPASVAETSGAIIA 287  
DB 234 ISNKAIISFINNSVTSATGATGATCYSSATSAPKPVLTLSDNGLNFIQTATISGAIYT 293  
QY 288 KKLALSSGGFTPELRN-VSATPKGALSIDASGELISAETGNTTFYRNTLTT-TGST 345  
DB 294 DNLVSSGGPTLFFKNNSAIDTAAPLGAIAIDSGSLISALGGDITFGNTVVKASSS 353  
QY 346 DPEKRAINIG-SNGKPELRRAKNTTFEYDPTSEGTS--SDVYKINNGSAGALNPYQ 402  
DB 354 OTTTRNSINIGNTAKIVQLRASQGNITFYDPTITSTIALSDALNLNGPDLAQPAYQ 413  
QY 403 GTILFSGETTLADLKVADNLKSSFTQPVLSGKLLLOKGYLTLESTFSQEAISLLGMD 462  
DB 414 GTLVFSGEKLSEAEAAEDNLKSTIQPQLTAGQGLSKGVTLVAKSFSQSGSTLLMD 473  
QY 463 SGTTLSTGSGITITTLGIVNDSGLKQVSLTAKASKNVIVSGCLNIDIEGNITYESH 522  
DB 474 AGTTLTETAG--ITINLVNLVDSLKETKATLKAQASGVTLVSGSLVDPGNYEDEV 532  
QY 523 MFSDHDLFSLKITYADVADVTVDVDSLLPVAEDPNSYFGQGNVMTTDTATNKE 582  
DB 533 SWNPQVFSCLTIT-ADPPANIHITDLAADPLEKPIHWGQGNALMSQEDTATKSA 590  
QY 583 ATATWTKTGFVSPERKSLAVCNTLWGVFTDIRSLQOLVEIGATGNEHKQGFVSSMTNF 642  
DB 591 AITLWTKTYNPNBERGTLVANTLWGSFVDVRSIQVLATKVRQSGETRGATCEISNF 650  
QY 643 LKKTGDENRKGRHTSGYVIGGSAHTPKDILFTFAFCHLPARDKCFIAHNSRYTGGT 702  
DB 651 FHKDSFKIKKGRPHISAGYVVGATTTLASDNLITTAFCOLFGKDRDHPINKRASAAYAS 710  
QY 703 LFFKSHHTLQPNVYLRGAKFSESAIEKFPREIPLALVOVSPFSHSDRMETHYSLPE 762  
DB 711 LHLQHLATLSSPBLVY--LPQSES-----EQVLFAQISYISKNTMKTYTQAPK 761  
QY 763 SEGWSNECIAGIGLDLPFLVSNPHLPFKTEIPQKMEVMYVVSQNSFPRESSD-GRGFS 821  
DB 762 GESSWVNDCALEIASLPLHTALSHGCLPHAFPIKVAASYIHQDSFEBRNTTLVRSD 821  
QY 822 IGRLLNLSPVQAKPYQDIDGSYYTDSLGFVSDVYRNNPOSTATVLSVPSDWKTRGN 861  
DB 822 SGDLIVSVPIGITFERFSRNERASYEATVIYADVARKNPCTCTALLINTSMKTTGTN 861  
QY 882 LSRQAFILAGSNVYNVNSCELFGYAMLELRGSSRVYNDVDTKURF 928  
DB 882 LSRQAGIGRAGIFVAPSPNLEVTSLNLSWELRGSRSKYNADLGKQFQF 928  
RESULT 6  
ID 0823W9\_CHLCV PRELIMINARY; PRT; 926 AA.  
AC 0823W9;  
DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)

DT 01-MAR-2004 (TRENBLREL. 26, last annotation update)  
 DE Polymorphic outer membrane protein G family  
 DE protein/autotransporter.  
 GN OrderedlocusNames=CCA00284;  
 OS Chlamydia caviae.  
 CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=83557;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GPIC;  
 RX MEDLINE=2256155; PubMed=12682364; DOI=10.1093/nar/gkh321;  
 RA Read T.D., Myers G.S.A., Brumham R.C., Nelson W.C., Paulsen I.T.,  
 RA Heidelberg J.F., Holtzaple E.K., Khouri H.M., Federova N.B.,  
 RA Carty H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.J.,  
 RA White O., Salzberg S.L., Heia R.-C., McClarty G., Rank R.G.,  
 RA Bavoil P.M., Fraser C.M.;  
 RT "Genome sequence of Chlamydia caviae (Chlamydia peitacti GPIC):  
 RT examining the role of niche-specific genes in the evolution of the  
 RT Chlamydiaceae.";  
 RL Nucleic Acids Res. 31:2134-2147(2003).  
 DR EMBL; AE016995; AAP05035.1; -; Genomic\_DNA.  
 DR TIGR; CCA00284; -; C:outer membrane, IEA.  
 DR GO; GO:0019867; C:outer membrane, IEA.  
 DR InterPro; IPR006315; Autotransporter.  
 DR InterPro; IPR005546; Auto\_transbeta.  
 DR InterPro; IPR011427; Chlammp M.  
 DR InterPro; IPR003368; Chlamydia\_pmp.  
 DR InterPro; IPR006626; Pbh1.  
 DR Pfam; PF03797; Autotransporter; 1.  
 DR Pfam; PF07548; Chlammp\_M; 1.  
 DR Pfam; PF02415; Chlam\_pmp; 6.  
 DR SMART; SM00710; Pbh1; 4.  
 DR TIGRFAMS; TIGR01414; autotrans bar1; 1.  
 DR TIGRFAMS; TIGR01376; pomp\_repeat; 5.  
 KW Complete proteome.  
 SQ SEQUENCE 926 Aa; 98213 MW; 0E1062E0778658B2 CRC64;

Query Match 37.5%; Score 1791; DB 2; Length 926;  
 Best Local Similarity 40.5%; Pred. No. 1e-90;  
 Matches 382; Conservative 166; Mismatches 363; Indels 32; Gaps 16;

QY 1 MKTSPWLVSSVLA--FSCHQSLANELLSPDDFNGNIDSGTFPTKTA---TTPS 54  
 DB 1 MRPSLYKILISSTLIPLSFHSQVHAEVALTOESVLDA--GAFSPQSTSTAGTTYN 57  
 QY 55 LTGVDFEPEPKGPTLSDSCFKOTDNLTPLGNGSLTFPGFDAGTHAGAASTANKL 114  
 DB 58 VESDISIVDAGAAAMVSAAFVQTADDLTFKNGRSLAIENNVSGANFAGAIYVSADKTL 117  
 QY 115 TFSGFLSPDSSPTVTYTGQTLSSAGVLENIIRKLVAAGNFSTADGAIKASFL 174  
 DB 118 TLTDSTLSPFKKCPHTVNTGKAVKSGGALNLANNASILFNQNHNSADGAIKASRL 177  
 QY 175 TGTSGDALFSNNSSSTKGAIAITTAGARIANNTRYRLSNASTSGAIDEGTSLISN 234  
 DB 178 TGSSKEISFTTWTSTYKKGAIATGVANLSDQKVIIFSGTAVVNSGAVVAEANTTTAG 237  
 QY 235 NKFLYEEGNAKKT---GGAICNTKASGPELIIISNNKTLIPASNVAFETSGAIIHAKL 290  
 DB 238 NSAVFNNNAVTGTTDGGCGGAIHCKTGATPVLTIRDKVLLFKENTSAAGAIYADKL 297  
 QY 291 ALSGFEFLRNNVSSATPKGAISIDASGELISAETGNTTFVRNTLTGSTDTPKR 350  
 DB 298 YLTSGGPIVFNQKATNAAPKGAIGIANGECSTIAHGDITF--ENNLINATNATVYR 356  
 QY 351 NAININGSGKFTELPAANKHTIFPYDPITSEGTSSDVLKINNSAGALNPQGITLFSGE 410  
 DB 357 NAINIEGNGKEFVNLRAASGNLTLPYDPVVGSTADLLTIN--QAEGTKVYNGRIIFSGE 414  
 QY 411 TLTDELKVAADLKSSFTQPVSLGSKLLLOKGVLTLESTSPSGEGLLQMDSGTTLST 470  
 DB 415 KLTEDQTDADNLTQVTFQPIALAAAGELILKNGVEEAKVASQTAGSLILIDAGTKLSAK 474

QY 471 AGSITTNLGINVDSI-GLKQPVSLTAKASNKVYISGKLNILIDEGNIYESHMFHDOL 529  
 DB 475 TEDVTILNLAINPNSIDGFKIAVIAVANAKN-VTVGAIGIIDPFGKFEYEDHKLNETLA 533  
 QY 530 FSLKITTVDADVTTNDISLIVPADDPNSEIFGPGQNVNMTTPTATKETA--TW 567  
 DB 534 LGGIQFSAKSI-TTIDVPS--TTTRSPAQHHGYGQNSLSWITNGSDPKQTAVFNM 589  
 QY 588 TKTGFVSPERKALVNTLTMGVFTDIRSLQOLVEIGA-TGMEHKQGFVWSMTNPLAK- 645  
 DB 590 NKGQVNPERRAPVNLNSMGSPFMDIRSLQDMESVDTLLETTRGLVWSGNGNLHMD 649  
 QY 646 TGDENRKGFRTISGYYIGGSAHTPPDOLFTEAFCHLPAPDKCFLAHNNSRTYGTLPF 705  
 DB 650 PSANENK-FRHISSGVYLGAITNTSOEDTLISVAFCOLFGDKXLYLAKNAANYAASIIYY 708  
 QY 706 KHSHTLQPVNYLGLAKPSESALIEKPREIPLALVOVVSFSSDNRMETHYSLPESG 765  
 DB 709 QHVSKEDDLTRLFNG---PNTCCSGFSKEIPLFLAQVYCHTNMMTTTYDPEVKG 764  
 QY 766 SMNECTIAGIIGDLDFVLSPNPPLPKTFIPQKVMVYVVSQNSPFESSDGRGFSIGRL 825  
 DB 765 SKGNDVYVALSLSVPIPIPT-HAFDVSAPFAKLQVVAHQDFEPTREGRTFESSDL 823  
 QY 826 LNSIPVGAKEVQGDIGDSTYYDLSGFVSDVYRNNPOSTATLWSPDSKIRGNLSRQ 885  
 DB 824 LNVSVPIGVFEKLVGKEKTAVDLTLMVYDVRHNPNCITGPAINDVMTLTATNLARQ 883  
 QY 886 AFLRGSNNVYVNSCELFGHYAMELRGSSRRNVNVGTRLP 928  
 DB 884 AFLIRAGNHIAVTSGFEMFSQFGFELRSSRRNVVDLAKAVSF 926

## RESULT 7

PMPI0\_CHLNP STANDARD; PRT; 928 AA.  
 ID PMPI0\_CHLNP STANDARD; PRT; 928 AA.  
 AC Q9RB65; O86163; Q9RB64; Q9S6P2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Probable outer membrane protein pmpl0 precursor (Polymorphic membrane  
 DE protein 10) (Outer membrane protein 5).  
 GN Name=pmpl0; Synonyms=omp5; OrderedlocusNames=CP0303, CPB0467;  
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
 CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=83558;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CWL029 / VR1310;  
 RX MEDLINE=20007584; PubMed=10539856;  
 RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,  
 RA Madsen A.S., Knudsen K., Falk B., Birke Lund S.;  
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their  
 RT role in immunopathogenicity.";  
 RL Am. Heart J. 138:S491-S495(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=AR39;  
 RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;  
 RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J.D., Uterback T.R., Berry K.J.,  
 RA Baas S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,  
 RA Dodson R.J., Gwinn M.L., Nelson W.C., Deboy R.T., Kolonay J.F.,  
 RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;  
 RT "Genome sequences of Chlamydia trachomatis Moyn and Chlamydia  
 RT pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=J138;  
 RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;  
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi T., Ouchi K.,  
 RA Shiba T., Ishii K., Hattori M., Kunara S., Nakazawa T.;

RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
 RT from Japan and CML029 from USA."  
 RL Nucleic Acids Res. 28:2311-2314(2000).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
 RC STRAIN=TW-183;  
 RA Geng M.W., Schumacher A., Mehldorfer I., Bensch K.W., Schaefer K.P.,  
 RA Schneider S., Pohl T., Essig A., Marx R., Meichers K.;  
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with  
 other Chlamydia strains based on whole genome sequence analysis."  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE OF 1-914.  
 RC STRAIN=CML029/VR-1310;  
 RX MEDLINE=99081766; PubMed=9864239;  
 RA Knudsen K., Madsen A.S., Mygind P., Christensen G., Birkelund S.;  
 RT "Identification of two novel genes encoding 97- to 99-kilodalton outer  
 membrane proteins of Chlamydia pneumoniae."  
 RL Infect. Immun. 67:375-383(1999).  
 CC -1- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)  
 CC (potential).  
 CC -1- SIMILARITY: Belongs to the PMP outer membrane protein family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: AJ133034; CAB37071.1; -; Genomic DNA.  
 DR EMBL: AE002192; AAF38160.1; -; Genomic DNA.  
 DR EMBL: BA000008; BAA98657.1; -; Genomic DNA.  
 DR EMBL: AE017158; AAP98398.1; -; Genomic DNA.  
 DR EMBL: AJ001311; CA04671.1; -; Genomic DNA.  
 DR PIR: G81591; G81591.  
 DR PIR: G86546; G86546.  
 DR PHCI-2DPAGE; O86163; -.  
 DR TIGR: CP0303; -.  
 DR InterPro: IPR005546; Auto\_transp\_beta.  
 DR InterPro: IPR006315; Auto\_transporter.  
 DR InterPro: IPR011427; Chlam\_PMP.  
 DR InterPro: IPR003368; Chlamydia\_PMP.  
 DR InterPro: IPR006626; Pdh1.  
 DR Pfam: PF03797; Autotransporter; 1.  
 DR Pfam: PF02415; Chlam\_PMP; 7.  
 DR Pfam: PF02548; Chlam\_PMP; 1.  
 DR SMART: SM00710; Pdh1; 4.  
 DR TIGRFAMS: TIGR01414; autotrans\_bar1; 1.  
 DR TIGRFAMS: TIGR01376; POMP\_repeat; 5.  
 KM Membrane; Multigene family; Outer membrane; Signal.  
 FT SIGNAL 1 25 Potential.  
 FT CHAIN 1 928 Probable outer membrane protein pmp10.  
 FT CONFLICT 305 305 Missing (in Ref. 4).  
 SQ SEQUENCE 928 AA; 97230 MW; 0590D5206A1DD0E1 CRC64;  
 Query Match 37.3%; Score 1785; DB 1; Length 928;  
 Best Local Similarity 40.4%; Pred. No. 2,2e-90;  
 Matches 385; Conservative 173; Mismatches 344; Indels 52; Gaps 18;  
 QY 1 MKTSIPVAVSSVLA--FSCHLQSLANEELSPDPSFGNIDSGTFTPKTSAT--TYSLT 56  
 DB 1 MKSGFSLVSLTACFTSCSTVPAATAENIGPSPDSGTSTNCTYTPKNTTGIDYTLT 60  
 QY 57 GDVFFYEPKGTPLSDSCFKQTTDNLTFLNGSHLTGCFIDAGHGAASSTANKLTF 116  
 DB 61 GDITLQNLGSAALTKGCFSDTTESSLFPAKGYSLSPLNKSAB--GAALSVTTDKNLSL 119  
 QY 117 SGFSLSPDSSPTVT--GQGTLSAGGVNLENIRLVAGNFTADGATKAGSFL 174  
 DB 120 TGRSFLFLAASPVTTPSGKAVKCGDLTFNNNTIIFKQDYCENGAISTKLSL 179  
 QY 175 TGRSGDALFSNNSST--KGAIAATTAGARIANNVTGVPFLSNIASTSGAIDECTST 231

DB 180 KNSTGISFEGNKSATGKKGAIICATGTVDTNNAPTFLFSNNIAEAGAINSTGNC 239  
 QY 232 LSNKKFLYPEGNAAKTT---GGAICNTKASGSPELIISNNKTLIPASNAVETSGAIHAK 288  
 DB 240 ITGNTSLVSENSVTITAGNGAL---SGDAVITSGQVTSFGNOAVANGAIIYAK 294  
 QY 289 KALSS--GGFTFLNNVSSATP-KGAIISIDASGELSIAETGNITFVRNTLTGTS 345  
 DB 295 KLTLAGGGGGISFNNNIVOGTTAGNGAISTILAAGECSISABAGDITFGNAIVAT-TP 353  
 QY 346 DTFKRAINIGSKRTFLRAKNHTIFFYDPTIS--GTSSVVLKINNSAGALPQY 403  
 DB 354 QTTKRNISIDIGTAKTTLNRAISGHSIFFYDPTTANTADSTDTLMLNKAADANSYDSC 413  
 QY 404 TILFSGETTLADLKYADNLKSSFTQPVLSGGKLLQGVTLSETPSGEAGSLGMD 463  
 DB 414 SLFSEKLSSEDAKADNLSTLKQPVTLTLAGNLVKKGVLTLDGTFQTAGSSVYMDA 473  
 QY 464 GTTLSTTAASTITTNIGINVDLSGLKQPVSLTAKGASNKVYSGKMLIDIEGNIYESHM 523  
 DB 474 GTTLKASTEBVTLTGSLIPVDSLGEKKVVIASAASKNVALSGPILLDNGNAVENHD 533  
 QY 524 FSHDQFLSLKTIVDADVDTNDISLIPYPADEPNSYFGQGMVNTTDTAT--NTK 581  
 DB 534 LKGTQDFSFVQLSA-LGTATTTDVP--VPTVATPTHGYQGTWGMVTDASTPKTK 589  
 QY 582 EATATWTKTGVPSPERKSAIVCNTLGMVFTDRSQQLVEIGATGMEHKQGFVWSMTY 641  
 DB 590 TATLAWNTGYLNPERRQGLVNPNSLMGFSBDIQAIQVIESALTLCSDRGMVAAGVAN 649  
 QY 642 FLAKTGDENRKGFRHTSGGVVIGSARTPKDDLFTFPAFCHLPARDKCFIAHNSRTYGG 701  
 DB 650 FLDKDKKGEKRRKRRHSGGVAIGAAQTCSENLISPAFQGLFSGSDPLVAKHDTYAG 709  
 QY 702 TLFFKASHTLQPONYTLRLGAKFSESAIEKFP---REIPLADVQVFSHSDNMTHTYT 758  
 DB 710 AFYIQHTEC-----SGFTIGCLDKLPRGSMHKLPLVLEGQIAYSHVSDLTLYYT 759  
 QY 759 SUPESGSMSENECIAGIGLDLPFLVSNPDP---LKFPTIPOMKVMYVVSQNSPFEES 814  
 DB 760 AYPEVKSGWGNNAFNNMLGAS---SHSYPEYLHCFDYAPYIKNLTYIIRDSSEKG 814  
 QY 815 SDGRGFSIGRLNLTSLPVGAKFVQGDIGSYTYDLSGFVSDVYRNNPOSTATLVMSPPS 874  
 DB 815 TEGRSFDDNLTFLSLPIGVKFKPSDCNDPFDLTLSVYPLDIRNDPCTTALVLSGAS 874  
 QY 875 WKIRGNLSRQAFLEFGSNVYVNSNCELFGHYAMELRGSSRYNVVDVGTCLRF 928  
 DB 875 WETVANNLARQALQVAGSHYAFSPWFVEVLGQFVEFRVSSRIYVNDLGKRFQF 928  
 RESULT 8  
 PMP8\_CHLPN STANDARD; PRT; 930 AA.  
 AC 09J2933; Q9RB66;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Probable outer membrane protein pmp8 precursor (Polymorphic membrane  
 protein 8) (Outer membrane protein 11).  
 GN Name=pmp8; Synonyms=omp11; OrderedlocusNames=CP00446, CP0307, CPB0463;  
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydiaophila.  
 OX NCBI\_TaxID=83558;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CML029 / VR1310;  
 RX MEDLINE=20007584; PubMed=10539856;  
 RA Christensen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,  
 RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;  
 RT "Molecular biology of Chlamydia pneumoniae surface proteins and their  
 RT role in immunopathogenicity."  
 RL Am. Heart J. 138:S491-S495(1999).

RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=CM1029;  
 RX MEDLINE=99206606; PubMed=10192388; DOI=10.1038/67716;  
 RA Kaiman S., Mitchell W.P., Marathe R., Lammell C.J., Fan J., Hyman R.W.,  
 RA Klinger L., Grimwood J., Davis R.W., Stephens R.S.,  
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";  
 RL Nat. Genet. 21:385-389(1999).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=AR39;  
 RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;  
 RA Read T.D., Burnham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 RA White O., Hickey E.K., Peterson J.D., Uetchback T.R., Berry K.J.,  
 RA Bass S., Linher K.D., Weidman J.F., Khouri R.T., Craven B., Bowman C.,  
 RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,  
 RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.,  
 RT "Genome sequences of Chlamydia trachomatis Mohn and Chlamydia  
 pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=J138;  
 RX MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;  
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.,  
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
 from Japan and CM1029 from USA.";  
 RL Nucleic Acids Res. 28:2311-2314(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=TW-183;  
 RA Geng M.M., Schumacher A., Muehlbauer I., Bensch K.W., Schaefer K.P.,  
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.,  
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with  
 other Chlamydia strains based on whole genome sequence analysis.";  
 RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)  
 (potential).  
 CC -1- SIMILARITY: Belongs to the PMP outer membrane protein family.  
 CC -1- SIMILARITY: Contains 1 autotransporter (TC 1.B.12) domain.  
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR EMBL; AJ133034; CAB37068.1; -; Genomic DNA.  
 DR EMBL; AE001627; AAD18590.1; -; Genomic DNA.  
 DR EMBL; AE002193; AAF38164.1; -; Genomic DNA.  
 DR EMBL; BA000008; BAA98654.1; -; Genomic DNA.  
 DR EMBL; AE017158; AAP98394.1; -; Genomic DNA.  
 DR PIR; A81591; A81591.  
 DR PIR; D72078; D72078.  
 DR PHCI-2DPAGE; Q92393; -.  
 DR TIGR; CP0307; -.  
 DR InterPro; IPR005546; Auto\_transpbeta.  
 DR InterPro; IPR006315; Autotransporter.  
 DR InterPro; IPR01427; ChlamPMP\_M.  
 DR InterPro; IPR003368; Chlamydia\_PMP.  
 DR Pfam; PF03797; Autotransporter; 1.  
 DR Pfam; PF02415; Chlam\_PMP; 6.  
 DR Pfam; PF07548; ChlamPMP\_M; 1.  
 DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
 DR TIGRFAMs; TIGR01376; PMP repeat; 6.  
 KM Complete proteome; Membrane; Multigene family; Outer membrane; Signal.  
 FT SIGNAL 1 26 Potential.  
 FT CHAIN 27 930 Probable outer membrane protein pmp8.  
 FT VARIANT 177 177 T->A (in strain AR39, strain J138 and  
 strain TW-183).  
 FT SEQUENCE 930 AA; 97670 MW; 46A9B5E3BB913C4C CRC64;

Query Match 36.8%; Score 1761; DB 1; Length 930;  
 Best Local Similarity 41.7%; Pred. No. 4,7e-89;  
 Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;  
 QY 1 MKTSIRWVVSSTLAFASCHLQSLAN---BELSPDSEFNQNDISGFFPKTSA---TTY 53  
 DB 1 MKTPIHKLKLISSLTVPPI-LTSLATYGADASISPDSPFG-AGGSFFYKSTADANGTV 58  
 QY 54 SLTGDFVFEYFPGKGTPLSDSCFCQKTTDNLTLFGNGHSLTFEGIDAQTHAGAAASTTANRN 113  
 DB 59 VLSGNYIINDAGAGTALTGCCFFETTGDLTLFGKGYSPFNVDAGSNAGAAASTTADKA 118  
 QY 114 LTFSGFSLSPDSEPTTYTTGGCTLSAGGVNLENIRKLVVAAGNSTA---DGAIKKA 170  
 DB 119 LFTFGFSNLSFIAPGTVAAGKSTLSAGANLTLNGCTLFSQNVSNBANNNGAIITTK 178  
 QY 171 SFLTLTGSDALFNNSSSTKGAIAITTAGARIANNYGVYFLSNASTSGAIDDEGTS 230  
 DB 179 TLSISGNTSSITFTNSAKKLGALYSAAASISGNTGQVFNANNGETGGALGFAS 238  
 QY 231 ILSNKKFLYFEGNAAKTT---GGAICNTFASGSPBLIISNNKTLFASVNAETSGAIIHA 287  
 DB 239 SITQNSLFPSSGNTATDAAGKGAICYCKTGERTPLTISGKSLTFASNSVTGGALICA 298  
 QY 288 KKLALSSGGFTFLRNNV-SSATPKGCAISIDAGSLISAETGNTFYRNTLTTTGSTD 346  
 DB 299 HGDLISAAGPTLFSNNRCGNTAAGKGAIALIDSGSLSSANQGDITFGNLTITST-5AP 357  
 QY 347 TPKRNALINISGKCFELBAAKNHTIFFYDPTISSET-SSDYKINNGSAGALNPGYGT 405  
 DB 358 TSTRNALIYSSAKITNLRAAGOSIIFYDPLASNTTSGASDVLTINQPPNSLIDYSGTI 417  
 QY 406 LFGSETLTADDELTVADNLKSSFTQPVYLSGGKLLLOKGYLTBESTSPQSEAGSLMGDSGT 465  
 DB 418 VFSGEKLSADDEAQAANFTSILKQPLALASGTLALGNVELDVNGFTQREGSLTMQPGT 477  
 QY 466 TLSTAGSITTNLGNVDSGLKQPVSLTAKASKNVYSGKLNLDIEGNTIEGHHMS 525  
 DB 478 KLDADTEALISLTKLVNLSLALBGNKSVSIETAAANTITLTSLPVDQSDSGNFEYSHTT- 536  
 QY 526 HDQLFSL-LKITVDADVDTNVDISLIPVPAEDPNSEYGGQGMNMTTDTATNKCAT 584  
 DB 537 -NQAFTQPLVFTAAATASDIYIDALTSVQTPPEPHYIGQGWKATW-ADIST-AKSGT 593  
 QY 585 ATYTKTGFPVSPRKALVGNLTLMGVFTDIRSLQQLVEIGATGMEHKQGFVWSSMTNPLH 644  
 DB 594 MTWYTTGVNPNERRASVVPDLSMASFTDIRTLQQLMTSQANSIYQQRGLMAGTANFFH 653  
 QY 645 KTGDENKGRHTSGGYVIGGSAHTPRKDLFTPAFCHLPARDXOCFLAHNSRTYGGTLF 704  
 DB 654 KDKSGTQAFRRHKSYGIVIGGSAEDSESENFVAFCOLFGKDXDLFIVENTSHNYLASLY 713  
 QY 705 FKSHTLQPNYVRLGAKFSESAIEKPREIFLALDVQVSPFSHSDNBMETHYTSPESE 764  
 DB 714 LQHRALFG-----GLPMPSFGSITDMLKDQIPILMAQLSYSTIKNDMDTRTISPEAQ 766  
 QY 765 GSNMNEICIAGCIGLDLPFVLISNPHLPFKTFIPOMKVMYVVSQNSPFESSSDRGFSIGR 824  
 DB 767 GSWTNNSGALIEGSLALYLPKPAFPQGYFFFLKQAVYSRQNFESGABARAFDGD 826  
 QY 825 LNLSTIPVAKPVQGDIGDSYTDLSGFVSDYVRNNPOSTATLVNSPDSWKIRGGLSR 884  
 DB 827 LVNCSIPVGIRLEKISDEKKNFEISLAYIGDVARKPRSRSTLWVSGASWTSLCKNLAR 886  
 QY 885 QAFILRGSNNVYVNSNCELFGHYAMELRGSSRRNVNDVYGLKLF 928  
 DB 887 QAFLASAGSHLTLSPHEVLSGEAAYELRGSAAHYINVDGRLYSP 930  
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 PMP7\_CHLPPN STANDARD; PRT; 936 AA.  
 ID\_PMP7\_CHLPPN  
 AC Q92898; Q9J542; Q9J504;

DT 16-OCT-2001 (Rel. 40, Last Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-SEP-2005 (Rel. 48, Last annotation update)  
DE Probable outer membrane protein pmp7 precursor (Polymorphic membrane  
DE protein 7) (Outer membrane protein 12).  
GN Name=pmp7; Synonyms=omp12; OrderedLocustNames=CPH0445, CPH0308, CPH0462;  
OS Chlamydia pneumoniae (Chlamydia phylum: Chlamydiae)  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia phylum.  
OX NCBI\_taxid=83558;  
RN  
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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=CWL029;  
RC MEDLINE=998206606; PubMed=10192388; DOI=10.1038/7716;  
RA Kallman S., Mitchell W.P., Marathe R., Lammet C.J., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).  
RN  
RN  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=AR39;  
RC MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;  
RA Reed T.D., Burnham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J.F., Khouri H.M., Crahen B., Bowman C.,  
RA Bass S., Linher K.D., Weidman J.D., Knouri H.M., Crahen B., Bowman C.,  
RA Dodson R.J., Gwin M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,  
RA McCarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).  
RL  
RL  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=J138;  
RC MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).  
RL  
RL  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=TW-183;  
RC MEDLINE=20007584; PubMed=10539856;  
RA Christiansen G., Boesen T., Hjerno K., Dagaard L., Mygind P.,  
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;  
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity."; Am. Heart J. 138:S491-S495(1999).  
RL  
RL  
RN SUBCELLULAR LOCATION: Cell wall surface (elementary bodies) (potential).  
CC  
CC  
CC -I- SIMILARITY: Belongs to the pmp outer membrane protein family.  
CC -I- SIMILARITY: Contains 1 autotransporter (TC 1.B.12) domain.  
CC  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on items  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC  
CC EMBL; AE001627; AAD18589.1; -; Genomic DNA.  
CC EMBL; AE002193; AAF38165.1; -; Genomic DNA.  
CC EMBL; BA000008; BAA98653.1; -; Genomic DNA.  
CC EMBL; AE001718; AAP98393.1; -; Genomic DNA.  
CC EMBL; AJ133034; CAB37067.1; -; Genomic DNA.  
CC PIR; B81591; B81591.  
CC PIR; C72078; C72078.

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| DR  | PIR: C86546; C86546.   |
| DR  | PHCI-2DPAGE; Q92898; -.  |
| DR  | TIGR; CP0308; --.  |
| DR  | InterPro; IPR005546; Auto_transpibeta.                                 |
| DR  | InterPro; IPR006315; Autocransporter.                                  |
| DR  | InterPro; IPR011427; ChlamPMP M.                                       |
| DR  | InterPro; IPR003368; Chlamydia_PMP.                                    |
| DR  | pFam; PF03797; Autocransporter; 1.                                     |
| DR  | pFam; PF02415; Chlam_PMP; 7.   |
| DR  | pFam; PF07548; ChlamPMP M; 1.  |
| DR  | TIGRFAMs; TIGR01414; autocrans bartl; 1.                               |
| DR  | TIGRFAMs; TIGR01376; POMP repeat; 5.                                   |
| KW  | Complete proteome; Membrane; Multigene family; Outer membrane; Signal. |
| FT  | SIGNAL 1 23 Potential.   |
| FT  | CHAIN 24 936 Probable outer membrane protein pmp7.                     |
| FT  | CONFLICT 658 666 PTRHGFRRI -> EDNLRYRN (in Ref. 5).                    |
| FT  | CONFLICT 822 822 Y->H (in Ref. 1, 4 and 5).                            |
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| <br>  |  |
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| Best Local Similarity   | 39.9%; Pred. No. 1.7e-87;  |
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| OY  | 1 MKTSIPMVIVSSVLAFSCHQLQSILNEELSDSDSFNGCIDSGTF----TPKTSATYSLSL         |
| Dd  | 1 MKSSVSMLFFPSISILFFSLSLSIAVAEVLTIIDSSNNISIDS-NGTTTFVBSITTDAAAGTYSLSL  |
| OY  | 56 TGDAVFYEPEPK-GTPLSDSCFKQTMDLTLFGNHSLFFPGFIDAGTHAGAAAATT-ANKN        |
| Dd  | 60 LSDVSFQNAGLGIPLASGCFLAEGDULFPQGQHALKFAFINNGSSAGTVASTADKN            |
| OY  | 114 LTSPGSFILSPDSSPSTVT-TGGCTLSAGCAVMLENIRKLVAANGNSTADGAIKASF          |
| Dd  | 120 LLEPDFSRSLSIICPSLISPFGCALKSVNLISLTGNSQIIFTONFSSDNGGVINTQNF         |
| OY  | 173 LLTGTSGDALFSSNNSSST--KGALATTAGARIANNTRYVAFSLIASISGGAIDEGTS         |
| Dd  | 180 LLSGTSGPASFSRQAFTGKGAVVATGTTIENSPETVFSQNLAGSGGALYSTDNC             |
| OY  | 231 ILSNKPLEYPEGN---AAKTGCAICNTKASGSEPELLISNNKTLIFASNYAETSGAIH         |
| Dd  | 240 SITDNFOVIPGNSNAMEAQOGAICTTTDKI-VLTGNKULSFNNHTALTGYGAIS             |
| OY  | 287 AKKIALLSGGFTEFLRNNVSSATP--KGAI SIDASGELSLSAETGNIITVRNTLTGG         |
| Dd  | 298 GLAKVISAGGPTEL-QSNISGSSAGOGGCGAINIASAGELALSATSGDITF-NNNQVTNG       |
| OY  | 344 STDPKRNAINIGSKFTELRAKNRTIFYDDPTTSST--SSPVLKINNGSAGALNPX            |
| Dd  | 356 STST--RNAINI DTAKVTSIRAATGOSIYEYDPIVNGTAASDTDLNLINLADANSEIEY       |
| OY  | 402 OGTLIFSGETLTADELKVADVLLKSFPOVSLSGCKLLLGKGVLETSSFQSOAGSLIGM         |
| Dd  | 414 GGAIVFSGEKSLPEKAIAANVTSTIROPAVLANGDLVBRCGVITYFDLDIOSPESRLIM        |
| OY  | 462 DSGETLTSTAGSIITNLGINVDLSLKKOPVSLTAKGANRVIVSGKLNLIIDIEGNIYES        |
| Dd  | 474 DCGTTLSKEANLISLNGLAVALSSLIDGTNKAAALKTEADKNI SLSGRTIALIDBESSFYEN    |
| OY  | 522 HMFESHDLFSLLKITTVDADVDTNDISSLVVPADPNSEVEFGQGMVVMTTDTATNTK          |
| Dd  | 534 HNLSASTYPLLIELTT-AGANGTITLGLASTLLOEPETHYGQGMWL5MA-NATSSK           |
| OY  | 582 EATATMTKTGVSPSPERSALVCUTLLMGVFDNISLQOLVEIGATGMGHKGOFWWSMTN         |
| Dd  | 591 IGSINMWRTIGTIPPERKSUNPLNSMCNFIIDISINDLITKSSGEFFRELMISGLIAN         |
| OY  | 642 FLAKTGDENRKGFRRHSIGGYVIGSAHTPKDULETFAECHLFARDKOCFIAHNNSRTYGG       |
| Dd  | 651 FFYDSMPTRHGRFHISGGVALGITATTPABDOCLTAPCCQFARDRNHI TSKNHDTGYA        |
| OY  | 702 TLFFKHSHTL-QPONYELFLGAKSESBAIEKFPREIPLADVQVSSHSIDNMENHYSL          |



Db 711 SLVFHHTGFLDIANFL-WKATRAPVWLSEISQIILPSDPAKRSYLATDNHMKTYTND 769  
Qy 761 PSESGWSNCEIAGIGLDLPVLSNPHLPKFTPIPMKEMVYVYVONSFFESSDGRGF 820  
Db 770 SIIRKGRNDAFCADLGAISLPVIVSVY-LIKEVEPVVKQYIYAHQODYERAEGRAF 828  
Qy 821 SIGRLNLISIPVGAKEVQGDIGDSYTYDLSGFFVSDVYRNNPOSTATLVNSPDSWKIRGG 880  
Db 829 NKESELINVEIPIDGTFPDRSKSEKGYDTLIMYILDAVRRNPKQTSILASDANMAVYGT 888  
Qy 881 NLRSQAFLRGSNVYVNSNCELFHGYAMELRGSSRNRYVDVGTCLRF 928  
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0823X0\_CHLVCV  
ID 0823X0\_CHLVCV PRELIMINARY; PRT; 866 AA.  
AC 0823X0;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Polymorphic outer membrane protein G family  
DE protein/autotransporter.  
OS Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
NCBI\_TaxID=83557;  
RN NUCLEOTIDE SEQUENCE.  
RC MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;  
RA Read T.D., Myers G.S.A., Brunham K.C., Nelson W.C., Paulsen I.T.,  
Heideberg J.F., Holtzaple E.K., Khouri H.M., Federova N.B.,  
Carty H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.J.,  
Bavoli P.M., Frieser C.M.,  
"Genome sequence of Chlamydia pneumoniae (Chlamydia psittaci GPIC):  
RT examining the role of niche-specific genes in the evolution of the  
RT Chlamydiaceae";  
RL Nucleic Acids Res. 31:2134-2147(2003).  
DR EMBL; AB016995; AAP05034.1; -; Genomic\_DNA.  
DR TIGR; CCA00283; -;  
DR GO; GO:0019867; C:outer membrane; IEA.  
DR InterPro; IPR006315; Autotransporter.  
DR InterPro; IPR005546; Auto transbeta.  
DR InterPro; IPR011427; ChlamPMP\_M.  
DR InterPro; IPR003368; Chlamydia\_PMP.  
DR Pfam; PF03797; Autotransporter; 1.  
DR Pfam; PF02415; ChlamPMP\_M; 1.  
DR Pfam; PF02415; ChlamPMP\_M; 5.  
DR TRFPMs; TIGR01414; autotrans bar1; 1.  
DR TRFPMs; TIGR01376; POMP\_repeat; 4.  
KM Complete proteome.  
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Query Match 33.4%; Score 1598; DB 2; Length 866;  
Best Local Similarity 37.5%; Pred. No. 4.6e-80;  
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Qy 1 MKTSPVWLVSSVLAFCSHLO-SLANEBLLSPDPSFNGNIDSGFTTPK--TSATYSLTG 57  
Db 1 MKHPVWLVSSVGLASTSLSPAFAVQETLNSDSYNNAATTDFAQTETTTGALEYTCGG 60  
Qy 58 DVFFPEPKGTPPLNSCFKQTDNLTFGNHSLTFGFIADACTAGAAASTTANKNLFFS 117  
Db 61 NVCTTYAKTTPPLTKSCFTEETLTFIGQGSICFDNITAKPAALIEVSAADTUSIS 120  
Qy 118 GFSILSPSSPTTYTTGQGTLSAGVNLKIRLVVAGNFSFADGAIKAGASFLITGT 177  
Db 121 GFSILSPSSPTTYTTGQGTLSAGVNLKIRLVVAGNFSFADGAIKAGASFLITGT 178  
Qy 178 SGDALFSNNSSSTKGAIATTAGARIANNVGRFLSNIASTSGAIDDEGTSILSNKF 237

Db 179 SVCANFIKNSDKKGAI----- 196  
Qy 238 LVEGNAATGGAIENTRKASGPELLISNNKTLIPASVVAETSGAIAHAKKLALSGGCF 297  
Db 197 -----YSDS-----NQLENNQMLFSEHTSREBGAIYAKKLALISGGGP 237  
Qy 298 TEFLRNVS-SATPKGAISI-DASGELSIAETGNTITVRNTLTGSGTDTPKRNAINI 355  
Db 238 TLFSNNSTSKADPKGAICIDADSECSLTAEENGIIIPDGKIIITYGTPST-KRNSIDL 296  
Qy 356 GSNKGTTELRAAKNHTIFPYDPTTSRGTSDVLKINNSAGALNPQGTILPSGFTLTD 415  
Db 297 GSGKFSQLRARDGFGVFPYDPIANNGSTDTLEIKADGAA--TYSGLIVFSGEKLTD 354  
Qy 416 ELKVADNLKSSFTQPVLSGKLLQKGVLTLESTSPQAGSLGMDSGTTLSTTASIT 475  
Db 355 EKQVTDNLKLSFFQPLTVSGSGSVLKNQVTSAGKQITQSGGA-IEMDAGTNTLTSTEDIS 413  
Qy 476 ITNLGINVDSL--GLKQPVSLTAKGASKVYSGKLNIDIEGNIYESHMFMSHQLF-S 531  
Db 414 LSNLVINTSLGGGVPPLAAQISABG-TWKSVTISSLNVDAQNGVEYVPVSTTEFPS 472  
Qy 532 LKITYDADVDVNTVDISLIPVAEDPNSEYFGQGMVNTTDTATNKEATATWTKTG 591  
Db 473 IIEAKANGTPTTPTTHLTD--HAPAAHYGIGQIMTTSWQGTATTSQALTLAMQQTG 529  
Qy 592 FVSPERKALVNTLMGFTDIRSLQQLVEIGATGMEHKQGFVWSMTNPLHKTGBNR 651  
Db 530 YNPNPERQGLVNTLMGSGSDVRAIQNLMDISVNADYQRGIMAGLANFLQSGTEWK 589  
Qy 652 KGRHTSGGVYIGGSAHTPKDILFTAFCHLPARDKOCFIAHNSSTYGGTLFPKSHTL 711  
Db 590 RKRRHNSAGVIGAVYAKTISDDVFSAAFCQLFRDXYVVSKNNSIYVGSIIYHGFWS 649  
Qy 712 QPNYV---RLGAKSSESAIEKPREIPLADVOYFSGSDRMEHTYS-----L 760  
Db 650 DAVDNLQSTLG-----AQAPLVLAQULTSHTSNDKMTNTTKAAPQGVY 696  
Qy 761 PSESGWSNCEIAGIGLDLPVLSNPH-PLKFTPIPMKEMVYVYVONSFFES-SSDGR 818  
Db 697 PELKGMQNDGCFVELGATVP--IESPYSGLFMYSPPLRFQVLVAHQEDFKENNSTEGR 754  
Qy 819 GFSIGRLNLISIPVGAKEVQGDIGDSYTYDLSGFFVSDVYRNNPOSTATLVNSPDS--WK 876  
Db 755 YFESSDLTNISMPDIGKFERFSDNDIASVNTLAVAPDLVRSNPDKTSLVSPTAVWL 814  
Qy 877 IIRGNLSRQAFILRGSNVYVNSNCELFHGYAMELRGSSRNRYVDVGTCLRF 928  
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ID 09RB71\_CHLPN PRELIMINARY; PRT; 772 AA.  
AC 09RB71; 07BX22;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Pmp\_3 (Outer membrane protein 5).  
GN Name=pmp\_3\_2; OrderedLocustNames=Cpb0018;  
OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
OC Bacteria; Chlamydiaceae; Chlamydiales; Chlamydiaceae; Chlamydia.  
NCBI\_TaxID=83558;  
RN NUCLEOTIDE SEQUENCE.  
RC STRAIN=J138;  
RC MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;  
RA Shiba T., Ishii K., Hattori M., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
Shiba T., Ishii K., Hattori M., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
"Comparison of whole genome sequences of Chlamydia pneumoniae J138  
RT from Japan and CWL029 from USA";  
RL Nucleic Acids Res. 28:2311-2314(2000).



RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=TW-183;  
 RA Geng M.M., Schumacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,  
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.,  
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with  
 RT other Chlamydia strains based on whole genome sequence analysis."  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BA000008; BAA98226.1; -; Genomic DNA.  
 DR EMBL; AE017157; AAP97951.1; -; Genomic DNA.  
 DR PIR; H86492; H86492.  
 DR GO; GO:0019867; C:outer membrane; IEA.  
 DR InterPro; IPR06315; Autotransporter.  
 DR InterPro; IPR00546; Auto\_transpbeta.  
 DR InterPro; IPR01427; ChlamPMP\_M.  
 DR InterPro; IPR00368; Chlamydia\_PMP.  
 DR Pfam; PF03797; Autotransporter; 1.  
 DR Pfam; PF07548; ChlamPMP\_M; 1.  
 DR Pfam; PF02415; Chlam\_PMP; 6.  
 DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
 DR TIGRFAMs; TIGR01376; POMP\_repeat; 6.  
 DR SEQUENCE 772 AA; 82931 MW; 484FC5D635801EB CRC64;  
 SQ  
 Query Match 33.3%; Score 1591; DB 2; Length 772;  
 Best Local Similarity 42.7%; Pred. No. 9,7e-80;  
 Matches 337; Conservative 146; Mismatches 275; Indels 32; Gaps 14;

Db 644 LQFVAHQBFKQGTAREBFSSRLVNLALPIGRFDKESDCDA-TYNLTGTVDLV 702  
 Qy 859 RNNPOSTATLVMSPDMSKIRGNLSRQAFLLRGSNNVYVNSNCELGHYAMELRGSSRY 918  
 Db 703 RSNPDCTTLIRISGDSWKTFGTNLALQALVLRAGNHFCTNSNFAPRSQSFELRGSSRY 762  
 Qy 919 NVDVGTFLRP 928  
 Db 763 NVDLGAQYQF 772  
 RESULT 12  
 ID P77792 CHLAB  
 AC P77792; O5LSP5;  
 DT 01-FEB-1997 (T-EMBLrel. 02, Created)  
 DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)  
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
 DE POMP90B precursor (POMP90A precursor) (Polymorphic outer membrane  
 DE protein).  
 GN Name=pomp17G; Synonyms=pomp90B; OrderedLocusNames=CAB598;  
 OS Chlamydia abortus  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia  
 OC NCBI TaxID=83555;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=826/3;  
 RX MEDLINE=98187897; PubMed=9529048;  
 RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;  
 RT "Molecular cloning and characterization of the genes coding for the  
 RT highly immunogenic cluster of 90-kilodalton envelope proteins from the  
 RT Chlamydia psittaci subtype that causes abortion in sheep."  
 RL Infect. Immun. 66:1317-1324(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=826/3;  
 RX MEDLINE=96406378; PubMed=8810511; DOI=10.1016/0378-1097(96)00281-9;  
 RA Longbottom D., Russell M., Jones G.E., Laine F.A., Herring A.J.;  
 RT "Identification of a multigene family coding for the 90 kDa proteins  
 RT of the ovine abortion subtype of Chlamydia psittaci."  
 RL FEMS Microbiol. Lett. 142:277-281(1996).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=826/3;  
 RX PubMed=15837807; DOI=10.1101/gr.3684805;  
 RA Thomson N.R., Yeates C., Bell K., Holden M.T.G., Bentley S.D.,  
 RA Livingstone M., Cerdano-Parraga A.-M., Harris B., Doggett J.,  
 RA Omond D., Mungall K., Clarke K., Felwell T., Hance Z., Sanders M.,  
 RA Quail M.A., Price C., Barrett B.G., Parkhill J., Longbottom D.;  
 RT "The Chlamydia abortus genome sequence reveals an array of  
 RT variable proteins that contribute to interspecies variation."  
 RL Genome Res. 15:629-640(2005).  
 DR Genome Ref. 15:629-640(2005).  
 DR EMBL; U65943; AAC15924.1; -; Genomic DNA.  
 DR EMBL; U65942; AAC15922.1; -; Genomic DNA.  
 DR EMBL; CR848038; CAH64045.1; -; Genomic DNA.  
 DR GO; GO:0019867; C:outer membrane; IEA.  
 DR InterPro; IPR00546; Auto\_transpbeta.  
 DR InterPro; IPR006315; Autotransporter.  
 DR InterPro; IPR01427; ChlamPMP\_M.  
 DR InterPro; IPR00368; Chlamydia\_PMP.  
 DR Pfam; PF03797; Autotransporter; 1.  
 DR Pfam; PF02415; Chlam\_PMP; 4.  
 DR Pfam; PF07548; ChlamPMP\_M; 1.  
 DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
 DR TIGRFAMs; TIGR01376; POMP\_repeat; 3.  
 KW Complete proteome; Signal.  
 FT SIGNAL 1  
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D 1 MKHVVWVFLVSSSL-FASNSLSFANDQFALTPEDSYNGVNTSEFPVKEHSSSTYTC 59
QY 57 GDFVFEFGKTPYSDSCFKQTTNLTFLNGHSLTGFGL-DAGTHAGAAASTTANKLT 115
D 60 GNVCSIFAGKDSGKKSCEF-SATDNLTFPLGNGYTLCEFDNITTTTASNCGAIVNQGCGTLG 118
QY 116 FSGSLLSFDSSEPTVTYTGCTLSSAGVNLNIRKLVVAGNSTDAGAIKASFLLT 175
D 119 ISGFSLSFCAYCPGCT-----TG-----GAIQKNGTTLKDN 151
QY 176 GTSGDALFSSNNSSSTKGAIATTAGARIANTGYVRFPSNIASSTGGAIDDEGTSILSN 235
D 135 -----TG-----GAIQKNGTTLKDN 151
QY 236 KFLYPEGNAAKTTGCAICNTYASGSPELIISNNKTLFASVVAETSGAIIHAKKLALSSG 295
D 152 SSLVFHKKSCSTAEAGAI-QCKSSDAELKINNQNLVSENSSTSKGGAIVADKLTLVSG 210
QY 296 GFTEFLRNNSV-ATPKGAISI--DASGELSLAETGNITFVRN-TLTTGSTDTPKRNA 352
D 211 GPTLFSSNSVNSGSPKGAISIKDSSECSLTADLGDITDGKIKITSGSSSTVTRNS 270
QY 353 INISNGKFTELRAAKNHTIFFYDPTSEGTSDVLKINNSAGALNPYQGTILFSGRTL 412
D 271 IDLGT-GKFTKLRAADGFGIFFYDPT--GGSDDELINNKET--VDYTKIYFSGK 324
QY 413 TADEIKVADNLKSSFTQPVSLSGKLLIQKVTLESTFSQDAGSLGMDSGTTLSTAG 472
D 325 SDEEKARAEMLASTNQPIITLSAGSLVAKDVSVAQVTOEAGSTVMDGTTLQTPSS 384
QY 473 ---STTNLGINVSL---GLKQPVSLTAKGASKVIVSKLNLIDEGNIVESHMSH 526
D 385 GGETITLNLNLINIASLGGGGTSPAKIATYNTASQAITINA-VNLVDAGNAVEPIIAT 443
QY 527 DQFLSLKITVADVDVTWVDISSLIPVPAED-----PMSSEYGFQOGMMVNTTDTATNTK 581
D 444 SKPFLAIYATINA-----SYTQPTDNLTVNVPPTHGYGQNMVTVWDTETATKT- 493
QY 582 EATATWTKTGVPSPERKSALVCTLWGVFTDIRSLQOLVEIGATGMEHKOGFWVSSMTN 641
D 494 -ATLWTEQTVSPNEROGPLVPNTLWGAFSDLRAIQMLMDISVNGADYHNGFWVSGIAN 552
QY 642 FLHKTDENRKGFRTSGGVYVIGSAHTPKDGLTFEAFCHLFAHDKDFIAHNSRTYGG 701
D 553 FLHSGSDTKRFRNSAGYALGVYAKTPSDIFSAACQLFGKDKYLVSSNNANITAG 612
QY 702 TLEFFGH-SHTLQPOVYLRILGRAKFSESAIEKPREIPLADVOVFSHSDRMETHY--- 757
D 613 SLIYGHISYWSAMQULLQ-----NTIGAAPLVIANQLTYCHASNDKMTMTT 661
QY 758 -----TSLPESEGSNSNECIAGIGLIDLPVLSNPHLPFKTFIPQMKVEMVYVSONSFE 812
D 662 YAPRKTYAEIRKGDWNCDFVELGATVP-IQTESSLLFDMYSPLFKQLVHTHDDPE 720
QY 813 SSSD-CRGFSIGRLNLSTPVGAKFVQGDIGDSTYVYDLSGFPVSIVYNNPQSTLTAMS 871
D 721 NNSDGRYPSSNLTNLSLPIGIKFERPANNDTASYHTAAVSPIVASNPDCSTSLVS 780
QY 872 PDS--WKIRGNLSRQAFLLRGSNNYVNSNCELFGHAMLELRSRMYNVAVGTAKLP 928
D 781 PDSAAVWTKANLALSAFNLQAGNVLISLHNIETISQGFELRSGSRVYNDLGSKIQF 839

RESULT 13
082205 CHLCV PRELIMINARY; PRT; 841 AA.
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
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DE Polymorphic outer membrane protein G family
DE protein/autotransporter.
GN OrderedLocNames=CCA00624;
OS Chlamydia caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
RA Read T.D., Myers G.S.A., Brunham R.C., Neilson W.C., Paulsen I.T.,
RA Heidelberg J.F., Holtzapfel E.K., Khouri H.M., Federova N.B.,
RA Carey H.A., Umayam L.A., Haft D.H., Peterson J.D., Beaman M.D.,
RA White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G.,
RA Bayoili P.M., Fraser C.M.;
RT "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae."
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AE016996; AAF05366.1; -; Genomic_DNA.
DR TIGR; CCA00624; -.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto transpbeta.
DR InterPro; IPR011427; ChlamPMP_M.
DR Pfam; PF03797; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
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DR Pfam; PF02415; ChlamPMP; 4.
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DR TIGRFAMs; TIGR01376; POMP_repeat; 3.
KW Complete proteome.
SQ SEQUENCE 841 AA; 90411 MW; 21A9ED16E0D7C65D CRC64;
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QY 1 MKTISPVWLVSV--VLAFSCHLQSLANBELSPDSEFGNIDSGTFTPKSAT--TYSLTG 57
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QY 58 GDFVFEFGKTPYSDSCFKQTTNLTFLNGHSLTGFGLDAGTHAGAAASTTAN-KNLT 116
D 60 GNVCSIFAGKDSGKKSCEF-SATDNLTFPLGNGYTLCEFDNITTTTASNCGAIVNQGCGTLG 118
QY 61 NVCITVAGTKTTLKSCFETETENLTFLGQVSLCEFDNITTA-TAKPAALIEVSNNDTL 119
D 117 SGRSLSFDSSEPTVTYTGCTLSSAGVNLNIRKLVVAGNSTDAGAIKASFLLTG 176
QY 120 SGRSLSFDSSEPTVTYTGCTLSSAGVNLNIRKLVVAGNSTDAGAIKASFLLTG 176
D 120 SGRSLSFDSSEPTVTYTGCTLSSAGVNLNIRKLVVAGNSTDAGAIKASFLLTG 176
QY 177 TSGDALFSSNNSSSTKGAIATTAGARIANTGYVRFPSNIASSTGGAIDDEGTSILSNK 236
D 170 -----CDTGT-----NA 176
QY 237 FLYFEGNAAKTTGCAICNTYASGSPELIISNNKTLFASVVAETSGAIIHAKKLALSSG 296
D 177 ELKEFG-----NXYLLFSGNSSOQEGGAIYAKKLSTISG 211
QY 297 FTEFLRNNSV-SATPKGAISI--DASGELSLAETGNITFVRN-TLTTGSTDTPKRNA 354
D 212 PTFSSNSSTKAADPKGGAICADADSECLTBENGILIDGKIKITGTGTPST-KRNSID 270
QY 355 IGSNGKFTELRAAKNHTIFFYDPTSEGTSDVLKINNSAGALNPYQGTILFSGRTL 414
D 271 LGSGRKFSQLRARNGFVFYDPTLANNQSDTDLTEIKKAGAA--TVSGAIVFSGKLT 328
QY 415 DELKVDNLKSSFTQPVSLSGKLLIQKVTLESTFSQDAGSLGMDSGTTLSTAGSI 474
D 329 DEKQVTDNLKSFQKQPLTVSGSFVLKNGVTSAKQITQSGA-IEWDAGTNLTSTEDI 387
QY 475 TITNLGINVSL---GLKQPVSLTAKGASKVIVSKLNLIDEGNIVESHMSHDLF- 530
D 388 SLNMLVINTASLGGGVPVLAAGISAEQ-TNKSVTISLNLVDADNGEYEVFVSTTREP 446
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DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
DT 11-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE POMP91A (Polymorphic outer membrane protein).  
GN Name=pmp13G; Synonyms=pomp91A; OrderedLocustNames=CA8281;  
OS Chlamydia abortus.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxId=8555;  
RN  
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RC STRAIN=S26/3;  
RX MEDLINE=98187897; PubMed=9529048;  
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;  
RT "Molecular cloning and characterization of the genes coding for the  
RT highly immunogenic cluster of 90-kilodalton envelope proteins from the  
RT Chlamydia psittaci subtype that causes abortion in sheep.";  
RL Infect. Immun. 66:1317-1324(1998).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=S26/3;  
RX MEDLINE=96406378; PubMed=8810511; DOI=10.1016/0378-1097(96)00281-9;  
RA Longbottom D., Russell M., Jones G.E., Lainson F.A., Herring A.J.;  
RT "Identification of a multigene family coding for the 90 kDa proteins  
RT of the ovine abortion subtype of Chlamydia psittaci.";  
RL FEMS Microbiol. Lett. 142:277-281(1996).  
RN  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=S26/3;  
RX PubMed=15837807; DOI=10.1101/gr.13684805;  
RA Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,  
RA Livingston M., Cerdano-Tarraga A.-M., Harris B., Doggett U.,  
RA Ormond D., Mungall K., Clarke K., Feltwell T., Hance Z., Sanders M.,  
RA Quail M.A., Price C., Barrett B.G., Parkhill J., Longbottom D.;  
RT "The Chlamydia abortus genome sequence reveals an array of  
RT variable proteins that contribute to interspecies variation.";  
RL Genome Res. 15:629-640(2005).  
DR EMBL; U65942; AAC15921.1; -; Genomic DNA.  
DR EMBL; CR848038; CAH63731.1; -; Genomic DNA.  
DR GO; GO:0019867; C:outer membrane; IEA.  
DR InterPro; IPR005546; Auto\_transbeta.  
DR InterPro; IPR006315; Auto\_transbeta.  
DR InterPro; IPR011427; ChlamPMP\_M.  
DR InterPro; IPR003368; Chlamydia\_PMP.  
DR Pfam; PF03797; Autotransporter; 1.  
DR Pfam; PF02415; Chlam\_PMP; 3.  
DR Pfam; PF07548; ChlamPMP\_M; 1.  
DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
DR TIGRFAMs; TIGR01376; POMP\_repeat; 3.  
KW Complete proteome.  
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QY 53 YSLGDAVFVEYBPG-KGTPLSDSCFQKQTDNLTFLNGHSLTFEGIDA-GTHAGAAASTTA 110  
DB 58 YTCGNICIAAGLDGSGLSGSCFTDTGNLSFLDNGYTLCPDNTTSSHPGALSVSGT 117  
QY 111 NKNLTFSGFSLLSPDSBSTVTVTGQGLSSAGVNLNIRKLVVAGNFSADGALKGA 170  
DB 118 NKTLDISGFSLFSCAYCP----- 135  
QY 171 SFLTGTSGDALFSNNSSTKGAATATAGARIANNNGVRFSLNIASTSGAIDDEGTS 230  
DB 136 -----FGA-----TGY-----GAIKAVANT 150

QY 231 ILSNNKFLYFEGNAAKTTGGAICNTKASGSPELLISNNKTLIFASVVAETSGGAIHAKKL 290  
DB 151 TIDNNSLVFHKKCSITGEGGALICQKASSSBAELKINNQNVLFAENSSSSGGAIVADKL 210  
QY 291 ALSSGGFTFLRNNSVSAIPKGAISI-DASGSLISAETGNTTFYRN-TLTTGTGTDTP 348  
DB 211 TIVSGGPTFLSNNVSASSPKGALICIKDSGGCSLTALGDITFDGNNIKITNGGSPV 270  
QY 349 KRAVINGSNKGFTELRANKNHTIFYPDPTSEGTSSDYLKINNGSAGALNPYQGTILPS 408  
DB 271 TRNSIDGSSGKTKLNAKEGFGIFFYDPT--GGSDDELINIKQRT---VDYTGAIIVS 325  
QY 409 GETLTADDELKVADNLKSFQPVSLSGKLLQKGYTLSTSFSGAGSLGMDGTTLS 468  
DB 326 GERLSBEKKVAANLKSDFQPLKIGSGSLILKDGVTLETKSPFTQTEGATVVMVLDLGTLLQ 385  
QY 469 TTG---SITITNLGINVDSLG---LKQPVSLTAGASNKVIVSGKMLIDIEGNIYES 521  
DB 386 TPSSGGETITLTLMLDINVASLGGGVAAPPKAYEATTESKVTITN-VNLVDNGNAFEY 444  
QY 522 HMFSDQLFSLKITYDADVDVTNVDISLIPVPAED-----PSEYGFQGMNVNMTTDT 576  
DB 445 PTLAAGOPFLAIEVRSGS-----SGSITKFTTULENTPTPTHYGYQGMVTVTKQGS 496  
QY 577 ATYTKKATATWTKTGFVSPERKSALVCNTLWGVFTDIBSLQQLVEIGATGMEHKGFVY 636  
DB 497 SAQEKATLWEGDTGVSPIBERQSLVPNTLWGSFSDIRAIQVLMIDISVAGADYHNGFVY 556  
QY 637 SSMTNPLHKTGDNKRGFRHTSGGYVIGSANTPKDDLFFACHLPFADKCFIAHNS 696  
DB 557 SGLGNFLHKSQSDTKKFRNNSAGYALGYAQTSPSDVPSAAFCQLFGKDKDLVGRNSS 616  
QY 697 RTYGGTLEFGHSHTLQPONYL--RLGRAKFSESAIEKPREIPLALDVQVSPSHSDNRW 753  
DB 617 TVYAGSIYHISYNTWTNTLQNTLG-----AARPLVNLQALACHSNM 663  
QY 754 EHY-----TSLPSEGSWSNECTIAGIGLDLPVLNSPHPLFKTFIPQKVENYVY 805  
DB 664 KTNMTDTYAPKTTYSEIKGDMGNDGFGVEFGAKAP--IETASILPDMVSPFYKDLVHA 721  
QY 806 SQNSFPSSSD-GRGSIQGLMLSTPYGAKFPQOGIDGSDYTYDLSGFFSDVYRNPNQS 864  
DB 722 HODPFKNNSDQGRYFESNNLTNLSMPTIGVLEKFSHKDTASYNLTLLAAPDIVRSNPD 781  
QY 865 TATLVSPDS--WKIRGNLSROAFLRGSNNYVNSNCELFGHYAMELRGSSRNYYVDV 922  
DB 782 TATLVSPDSAVVWTTKANLARAFTLQAGNYLALRNTELPSQFQFELRGSGRTYNI DL 841  
QY 923 GTKLRF 928  
DB 842 GSKIQF 847

Search completed: November 25, 2005, 14:19:44  
Job time : 153.033 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:10:51 ; Search time 97.6977 Seconds  
(without alignments)  
3968.830 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 4782

Sequence: 1 MKTSLPWLVSSVLAFLSCHL.....MEIRGSSRNRYNDVGTKEF 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1          | 4782   | 100.0       | 928    | US-10-312-273-115    | Sequence 115, App  |
| 2          | 4782   | 100.0       | 928    | US-10-282-122A-54681 | Sequence 54681, A  |
| 3          | 4782   | 99.8        | 949    | US-10-289-762-478    | Sequence 478, App  |
| 4          | 1855   | 38.8        | 928    | US-09-428-122-2      | Sequence 2, Appl   |
| 5          | 1802   | 37.7        | 926    | US-09-738-269-57     | Sequence 57, Appl  |
| 6          | 1802   | 37.7        | 926    | US-10-023-437-57     | Sequence 57, Appl  |
| 7          | 1794   | 37.5        | 928    | US-10-312-273-33     | Sequence 33, Appl  |
| 8          | 1794   | 37.5        | 928    | US-10-503-135-99     | Sequence 99, Appl  |
| 9          | 1784   | 37.3        | 928    | US-10-312-273-95     | Sequence 95, Appl  |
| 10         | 1763   | 36.9        | 930    | US-10-289-762-470    | Sequence 470, Appl |
| 11         | 1761   | 36.8        | 930    | US-10-312-273-45     | Sequence 45, Appl  |
| 12         | 1761   | 36.8        | 930    | US-10-282-122A-54680 | Sequence 54680, A  |
| 13         | 1758.5 | 36.8        | 927    | US-10-289-762-472    | Sequence 472, App  |
| 14         | 1734   | 36.3        | 936    | US-09-452-380-3      | Sequence 3, Appl   |
| 15         | 1734   | 36.3        | 936    | US-10-324-129-3      | Sequence 3, Appl   |
| 16         | 1734   | 36.3        | 936    | US-10-312-273-153    | Sequence 153, App  |
| 17         | 1734   | 36.3        | 936    | US-10-282-122A-54679 | Sequence 54679, A  |
| 18         | 1705   | 35.7        | 925    | US-09-452-380-4      | Sequence 4, Appl   |
| 19         | 1705   | 35.7        | 925    | US-10-324-129-4      | Sequence 4, Appl   |
| 20         | 1562.5 | 32.7        | 839    | US-09-738-269-23     | Sequence 23, Appl  |
| 21         | 1562.5 | 32.7        | 839    | US-10-023-437-23     | Sequence 23, Appl  |
| 22         | 1535   | 32.1        | 746    | US-10-312-273-19     | Sequence 19, Appl  |
| 23         | 1435.5 | 30.0        | 841    | US-10-312-273-139    | Sequence 139, App  |
| 24         | 1435.5 | 30.0        | 841    | US-10-282-122A-54677 | Sequence 54677, A  |
| 25         | 1353   | 28.3        | 922    | US-10-312-273-41     | Sequence 41, Appl  |
| 26         | 1353   | 28.3        | 922    | US-10-503-135-98     | Sequence 98, Appl  |
| 27         | 1348   | 28.2        | 922    | US-09-886-468-19     | Sequence 19, Appl  |

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| 28 | 1345   | 28.1 | 922  | US-10-289-762-15     | Sequence 15, Appl  |
| 29 | 1286   | 26.9 | 643  | US-10-289-762-474    | Sequence 474, Appl |
| 30 | 1284.5 | 26.9 | 973  | US-10-312-273-3      | Sequence 3, Appl   |
| 31 | 1278.5 | 26.7 | 973  | US-10-352-618-2      | Sequence 2, Appl   |
| 32 | 1144.5 | 23.9 | 1407 | US-10-312-273-31     | Sequence 31, Appl  |
| 33 | 1144.5 | 23.9 | 1407 | US-10-282-122A-54678 | Sequence 54678, A  |
| 34 | 1144.5 | 23.9 | 1407 | US-10-503-135-94     | Sequence 29, Appl  |
| 35 | 1132.5 | 23.7 | 597  | US-10-289-762-29     | Sequence 29, Appl  |
| 36 | 1130.5 | 23.6 | 671  | US-10-289-762-468    | Sequence 468, App  |
| 37 | 1102.5 | 23.1 | 1013 | US-10-467-534-9      | Sequence 9, Appl   |
| 38 | 1102.5 | 23.1 | 1013 | US-10-498-327-5      | Sequence 5, Appl   |
| 39 | 1102.5 | 23.0 | 1013 | US-10-498-327-81     | Sequence 81, Appl  |
| 40 | 1100.5 | 23.0 | 1013 | US-10-498-327-9      | Sequence 9, Appl   |
| 41 | 1100.5 | 23.0 | 1013 | US-10-498-327-13     | Sequence 13, Appl  |
| 42 | 1100.5 | 23.0 | 1013 | US-10-498-327-93     | Sequence 93, Appl  |
| 43 | 1098.5 | 23.0 | 1013 | US-10-498-327-1      | Sequence 1, Appl   |
| 44 | 1098.5 | 23.0 | 1013 | US-10-498-327-3      | Sequence 3, Appl   |
| 45 | 1098.5 | 23.0 | 1013 | US-10-498-327-83     | Sequence 83, Appl  |

ALIGNMENTS

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| RESULT 1  | US-10-312-273-115 |
| Sequence 115, Application US/10312273                         |                   |
| Publication No. US20040005667A1                               |                   |
| GENERAL INFORMATION:  |                   |
| APPLICANT: CHIRON SPA   |                   |
| TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE |                   |
| FILE REFERENCE: P025035W0                                     |                   |
| CURRENT APPLICATION NUMBER: US/10/312,273                     |                   |
| CURRENT FILING DATE: 2002-12-20                               |                   |
| PRIOR APPLICATION NUMBER: 0016363.4                           |                   |
| PRIOR FILING DATE: 2000-07-03                                 |                   |
| PRIOR APPLICATION NUMBER: 0017047.2                           |                   |
| PRIOR FILING DATE: 2000-07-11                                 |                   |
| PRIOR APPLICATION NUMBER: 0017983.8                           |                   |
| PRIOR FILING DATE: 2000-07-21                                 |                   |
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| PRIOR FILING DATE: 2000-08-07                                 |                   |
| PRIOR APPLICATION NUMBER: 0020440.4                           |                   |
| PRIOR FILING DATE: 2000-08-18                                 |                   |
| PRIOR APPLICATION NUMBER: 0022583.9                           |                   |
| PRIOR FILING DATE: 2000-09-14                                 |                   |
| PRIOR APPLICATION NUMBER: 0027549.5                           |                   |
| PRIOR FILING DATE: 2000-11-10                                 |                   |
| PRIOR APPLICATION NUMBER: 0031706.5                           |                   |
| PRIOR FILING DATE: 2000-12-22                                 |                   |
| NUMBER OF SEQ ID NOS: 664                                     |                   |
| SOFTWARE: SeqWin99, version 1.02                              |                   |
| SEQ ID NO 115   |                   |
| LENGTH: 928   |                   |
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| ORGANISM: Chlamydia pneumoniae                                |                   |
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Db 421 DNLSKSTFQPVSLGKGLLOKGYTLBSTSFQAGSLGMDSGTTLSTTAGSITITNIG 480
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Qy 601 ALVNCNTLMGVTFTDIRSLQOLVEIGATGMEHKQGFVWSSMTNLFHKTGDNKRGFRHTSGG 660
Db 601 ALVNCNTLMGVTFTDIRSLQOLVEIGATGMEHKQGFVWSSMTNLFHKTGDNKRGFRHTSGG 660
Qy 661 YVIGGSATPKDDI.FTFAFCHLPARDKOCFTAHNNSRTYGGTLPFKKSHTLQOPNYRLG 720
Db 661 YVIGGSATPKDDI.FTFAFCHLPARDKOCFTAHNNSRTYGGTLPFKKSHTLQOPNYRLG 720
Qy 721 RAKSESASIEKFPREIPLADVOVSFSHSDNRMETHTYSLPESSEGSMSNECIAGIGIDL 780
Db 721 RAKSESASIEKFPREIPLADVOVSFSHSDNRMETHTYSLPESSEGSMSNECIAGIGIDL 780
Qy 781 PFVLSNPHPLFKTPIPOKKEVEMVYVSQNSPFESSSDGSGFISIGRLNLSIVGAKFVOGD 840
Db 781 PFVLSNPHPLFKTPIPOKKEVEMVYVSQNSPFESSSDGSGFISIGRLNLSIVGAKFVOGD 840
Qy 841 IGDSTTYLSCGFVSDDVRRNPQSTATLWSPDSKIRGNLSQOAFILRGSNNYVYNSN 900
Db 841 IGDSTTYLSCGFVSDDVRRNPQSTATLWSPDSKIRGNLSQOAFILRGSNNYVYNSN 900
Qy 901 CELFGHYAMELRGSSRNYNVDVGTCLRF 928
Db 901 CELFGHYAMELRGSSRNYNVDVGTCLRF 928

RESULT 2
US-10-282-122A-54681
; Sequence 54681, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
```

```
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54681
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54681

Query Match 100.0%; Score 4782; DB 4; Length 928;
Best Local Similarity 100.0%; Pred. No. 4,1e-307;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKSISPVVSVSLASCHLOSLANELLSPDSEFNGNIDSGTFPTKATATYSLGDVF 60
Db 1 MKSISPVVSVSLASCHLOSLANELLSPDSEFNGNIDSGTFPTKATATYSLGDVF 60
Qy 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGSLTFGFLDAGTHAGAAATANKMLTFESGS 120
Db 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGSLTFGFLDAGTHAGAAATANKMLTFESGS 120
Qy 121 LLSFSSPSTVTYTGQGTSSAGGVLENIRKLVAGNFSTADGAIKGAFLITGSGD 180
Db 121 LLSFSSPSTVTYTGQGTSSAGGVLENIRKLVAGNFSTADGAIKGAFLITGSGD 180
Qy 181 ALFSNNSSSTKGAIATTAGARIANTGYVRFILSNIASTSGAIDDEGTSILSNKFLYF 240
Db 181 ALFSNNSSSTKGAIATTAGARIANTGYVRFILSNIASTSGAIDDEGTSILSNKFLYF 240
Qy 241 EGNAAKTTGGAICNTKASGSPPELLISNNKTLIFASNAVETSGAIIHAKKALSSGGTFEF 300
Db 241 EGNAAKTTGGAICNTKASGSPPELLISNNKTLIFASNAVETSGAIIHAKKALSSGGTFEF 300
Qy 301 LRNVSSATPKGAIISIDASGELSLAETGNITFVRNTLTTSSTDPKRNAINIGSNGK 360
Db 301 LRNVSSATPKGAIISIDASGELSLAETGNITFVRNTLTTSSTDPKRNAINIGSNGK 360
Qy 361 FTBLRAAKNHTIFPYDPTSEGTSSDVLKINNSAGALNPYOGTILFSGETLTADDELKVA 420
Db 361 FTBLRAAKNHTIFPYDPTSEGTSSDVLKINNSAGALNPYOGTILFSGETLTADDELKVA 420
Qy 421 DNLSKSTFQPVSLGKGLLOKGYTLBSTSFQAGSLGMDSGTTLSTTAGSITITNIG 480
Db 421 DNLSKSTFQPVSLGKGLLOKGYTLBSTSFQAGSLGMDSGTTLSTTAGSITITNIG 480
Qy 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNITYESHMFSDQLFSLKITVDAD 540
Db 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNITYESHMFSDQLFSLKITVDAD 540
Qy 541 VDTNVDISSLIPVPAEDPNSSEYFGQGMNVMTTDTATNTKEATATWTGTFVPSPERKS 600
Db 541 VDTNVDISSLIPVPAEDPNSSEYFGQGMNVMTTDTATNTKEATATWTGTFVPSPERKS 600
```

QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKOGFWVSMNTNPLAKTGDENRKGFPHRTSGG 660  
DB 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKOGFWVSMNTNPLAKTGDENRKGFPHRTSGG 660  
QY 661 YVIGSSAHTPKDGLTFPAFCHLPARDKDCFIANNSTRYYGTLFPKHSHTLQPNYLRIG 720  
DB 661 YVIGSSAHTPKDGLTFPAFCHLPARDKDCFIANNSTRYYGTLFPKHSHTLQPNYLRIG 720  
QY 721 RAFFSSAIEKPREIPLALDVQVFSHSDNRMETHYTSLPSEBSWSNECIAAGIGLDD 780  
DB 721 RAFFSSAIEKPREIPLALDVQVFSHSDNRMETHYTSLPSEBSWSNECIAAGIGLDD 780  
QY 781 PVLNSPHLPFTFTPIPOKMEVYVYSONSFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
DB 781 PVLNSPHLPFTFTPIPOKMEVYVYSONSFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
QY 841 IGDSTYDLSGFFVSDVYRNPNQSTATLVMSPDSWKIRGNSLRQAFLRGSNNYYNSN 900  
DB 841 IGDSTYDLSGFFVSDVYRNPNQSTATLVMSPDSWKIRGNSLRQAFLRGSNNYYNSN 900  
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928  
DB 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

## RESULT 3

US-10-289-762-478  
; Sequence 478, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 478  
; LENGTH: 949  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: 1...949  
; OTHER INFORMATION: Xaa=unknown or other  
; US-10-289-762-478

Query Match 99.8%; Score 4774; DB 4; Length 949;

Best Local Similarity 99.9%; Pred. No. 1.4e-306; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTISPMVLVSVLAFSCHLQSLANEELSPDPSFNGNIDSGTFTPTSAITYSLTGDFV 60  
DB 22 MKTISPMVLVSVLAFSCHLQSLANEELSPDPSFNGNIDSGTFTPTSAITYSLTGDFV 81  
QY 61 FYRPGKTPISDSCFKOTTNLTFLLNGHSLTRGFIDAGTHAAGAASTTANKULTTSGGS 120  
DB 82 FYRPGKTPISDSCFKOTTNLTFLLNGHSLTRGFIDAGTHAAGAASTTANKULTTSGGS 141  
QY 121 LLSFDSSTPTTYYTGGOTLSSAGVNLNRLVVGNFSTAGGAIKXGSPFLTGTSGD 180  
DB 142 LLSFDSSTPTTYYTGGOTLSSAGVNLNRLVVGNFSTAGGAIKXGSPFLTGTSGD 201  
QY 181 ALFSNNSSSTKGALATTAGARIANTGYVPLSNIASTSGAIDDEGTSILSNKFLYF 240  
DB 202 ALFSNNSSSTKGALATTAGARIANTGYVPLSNIASTSGAIDDEGTSILSNKFLYF 261  
QY 241 EGNAAKTTGACIANTYASGSPPELLISNNKTLIFASVNAETSGAIAKAKLALSSGGFTEP 300  
DB 262 EGNAAKTTGACIANTYASGSPPELLISNNKTLIFASVNAETSGAIAKAKLALSSGGFTEP 321

QY 301 LNNVSSATPKGALSIDASGELSLSAETGNITFVRNLTITTTGSDTPRKNAINISNGK 360  
DB 322 LNNVSSATPKGALSIDASGELSLSAETGNITFVRNLTITTTGSDTPRKNAINISNGK 381  
QY 361 FTLELPAKKNHTTFPPDPTTSEGTSDVLYKINNGSAGALNPYGGTLLFSGEITLTAELKXA 420  
DB 382 FTLELPAKKNHTTFPPDPTTSEGTSDVLYKINNGSAGALNPYGGTLLFSGEITLTAELKXA 441  
QY 421 DNLKSSFTQPVSLSGKLLLOKGVTLTESTSFQOBSGLGMDSGTLLSTAGSITITNLG 480  
DB 442 DNLKSSFTQPVSLSGKLLLOKGVTLTESTSFQOBSGLGMDSGTLLSTAGSITITNLG 501  
QY 481 INVDSLGLKQPVSLTAKGASNFYVSGKLNLIIDEGNIYESHMFSDQLFSLKITTVDAD 540  
DB 502 INVDSLGLKQPVSLTAKGASNFYVSGKLNLIIDEGNIYESHMFSDQLFSLKITTVDAD 561  
QY 541 VDTNNDISLIVPAEDPSEYGFQGNVNMVTTDTATNTKATATWKTGTGVPSPERKS 600  
DB 562 VDTNNDISLIVPAEDPSEYGFQGNVNMVTTDTATNTKATATWKTGTGVPSPERKS 621  
QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKOGFWVSMNTNPLAKTGDENRKGFPHRTSGG 660  
DB 622 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKOGFWVSMNTNPLAKTGDENRKGFPHRTSGG 681  
QY 661 YVIGSSAHTPKDGLTFPAFCHLPARDKDCFIANNSTRYYGTLFPKHSHTLQPNYLRIG 720  
DB 682 YVIGSSAHTPKDGLTFPAFCHLPARDKDCFIANNSTRYYGTLFPKHSHTLQPNYLRIG 741  
QY 721 RAKFSSAIEKPREIPLALDVQVFSHSDNRMETHYTSLPSEBSWSNECIAAGIGLDD 780  
DB 742 RAKFSSAIEKPREIPLALDVQVFSHSDNRMETHYTSLPSEBSWSNECIAAGIGLDD 801  
QY 781 PVLNSPHLPFTFTPIPOKMEVYVYSONSFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
DB 802 PVLNSPHLPFTFTPIPOKMEVYVYSONSFESSSDGRGFSIGRLNLISIPVGAKEVQGD 861  
QY 841 IGDSTYDLSGFFVSDVYRNPNQSTATLVMSPDSWKIRGNSLRQAFLRGSNNYYNSN 900  
DB 862 IGDSTYDLSGFFVSDVYRNPNQSTATLVMSPDSWKIRGNSLRQAFLRGSNNYYNSN 921  
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928  
DB 922 CELFGHYAMELRGSSRNRYNDVGTCLRF 949

## RESULT 4

US-09-428-122-2  
; Sequence 2, Application US/09428122  
; Publication No. US20030170259A1  
; GENERAL INFORMATION:  
; APPLICANT: Mardin et al.  
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND  
; FILE REFERENCE: 19721-007-019  
; CURRENT APPLICATION NUMBER: US/09/428,122  
; CURRENT FILING DATE: 1999-10-27  
; EARLIER APPLICATION NUMBER: 60/106,046  
; EARLIER FILING DATE: 1998-10-28  
; EARLIER APPLICATION NUMBER: 60/132,271  
; EARLIER FILING DATE: 1999-05-03  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 928  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; US-09-428-122-2

Query Match 38.8%; Score 1855; DB 3; Length 928;  
Best Local Similarity 42.7%; Pred. No. 1e-113;  
Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;

|    |     |   |         |     |
|----|-----|---|---------|-----|
| QY | 7   | MKSIIMWLVYSSVLASCSHLOSLAMEBLLSPDSENGINDGCTPEPTTS----            | ATTYSLU | 56  |
| Db | 1   | MSSEFKFVFTFALFP--LSMIATEYVUDSSASFDGN-KXGNFSVRESQEDACTYLLFK      |         | 57  |
| QY | 57  | GDVFFYE-VQKGTPLSDSCFKQTTDNLTFLGNGHSLTEGFIDAGTHGAAA-STTANKUL     |         | 114 |
| Db | 115 | TEGSEFLSPDSEPSITTYTGGOTLS-SAGVNLNENIKLVVAAGNESTAOGAIKASFL       |         | 173 |
| QY | 174 | LVTSGDALFENNSSSTSGGAIATAGARIANNTRYVFLNINASTGCAIDEGTILS          |         | 233 |
| Db | 118 | TFIGFSSLSFASPGSITTYGKAVASCSTGSLIKNVLSLFSKOFSTDNCGAIATAKTIS      |         | 177 |
| QY | 178 | LITGTHSALFSENTSSKKGAIQTSDALTTTNGOEVSFSDNTSSDGAALFTRASVTIS       |         | 237 |
| Db | 234 | NNKFLVF-----EGNAKTT-----GGAICTNTKASGPELIISSNKTLLFASNALETSGA     |         | 284 |
| QY | 238 | NNAKVSPIDMKVYGAASSSTTGDMGGAI CAYXTISDTKVTLGNQMLFSSNNTSTTGA      |         | 297 |
| Db | 285 | IHAKKIALSSGGTELELRNNVSSAT-PKGAISIDASELSLSAETGNITFVRNTLTG        |         | 343 |
| QY | 298 | IYVKKIELASGGTLTFSRNSVNGCAPKKGAIADISELSLSADSGIVFLGNTVIST-        |         | 356 |
| Db | 344 | STDPKRNAINISNCKFTELPAKXNHTFEPDPTT--SEGTSSDYLKINNGSAGALNPY       |         | 401 |
| QY | 357 | -TGTNBSSTIDLTSAKMTALRSAAAGRAIYFDPDPTTSSSTTYDVLKNETPADSLQY       |         | 415 |
| Db | 402 | QGTILFSGETLTADDELKVAIDNLKSFTPOVSLSGKLLLOKVLTLESTFSQEAGSLIM      |         | 461 |
| QY | 416 | TGNIIFFGKSLSTEAADSKNLTSLKQVTLSSGOTLSLKHGVTLQTOAFQOASRLHEM       |         | 475 |
| Db | 462 | DSGTTLSTTAGSTTTNGLINVDLSGLKOPVSLTKAGSNKYVSGKLNLDISGNIYES        |         | 521 |
| QY | 476 | DVGTTLLE-PADTSTINNLVINISSIDAKAKAKIETKASIKMLTSLGTTLLDPTGYEN      |         | 534 |
| Db | 522 | HMFSDHLPLEKITVDADVTNVDISSLIPAPADPNSKGEFGOQNN-VMMTDTPLNT         |         | 580 |
| QY | 535 | HSLRNPDSYDILELKASGTVTS----TATPDPIMGEKFEHGYQCTMCPYWGICASTT-      |         | 589 |
| Db | 581 | KEATATWTKTGFAPSEPERKSALVCNTLMGVFIDISLQOLVEIGATGEMHKQFWSSMT      |         | 640 |
| QY | 590 | --ATFNNTKTGYPNPERIGSLVPNSLWMAFIDISLHMYETNABEGQGRAPWACGLS        |         | 647 |
| Db | 641 | NFLHKTGDENRKGRPHRTSGGYIVIGSARTPKODLTFPAFCHLPARDKOCFLAHNNSSTYG   |         | 700 |
| QY | 648 | NFFHKOSTKTRRGEFRHLSGGYIVGGMILHTCSDKIIISAAFCQLFGRDHPYFAKKOQTVYG  |         | 707 |
| Db | 701 | GTLFPHKSHILOQONTLRLGRAKFSSSAIEKFPREIPLALDVQVFSFSDNRMRHTHTSL     |         | 760 |
| QY | 708 | GTLVYQNNEL-----YISL-PCCLARPCCSISVPTLEPVLFSGNLSYHTHDDLLTKTITY    |         | 761 |
| Db | 761 | PESEGSNSNECIAGGICLDLPVLSPNPHLFTFTIIPOMKEVWVYVYQNSPESSSDRGF      |         | 820 |
| QY | 762 | PTVYGSNGNSFLHFPFGARPICL-DESMALFQGYNPFMLQVYVHAGQGFQGTAREF        |         | 820 |
| Db | 821 | SIGGLNLISIPVGAKF-VQGDIGDSTYYDLSGFVYSDVYRNNPOSTATLWMSPDMSKIRG    |         | 879 |
| QY | 821 | GSSTLVMLALPIGIRFPEKESDCODA--TYNLTIGYTVLIVRSNPDCCTTLRLISGDSMKTFG |         | 879 |
| Db | 880 | GNLSROAFILRGSNVNYVNSCELPHGYAMELREKSSRRNNVDVGTKLAF               |         | 928 |
| QY | 880 | TNLARQALVIRAGNHFCFENSNFEAFQSFPELGRSSRRNNVDLGAKYOF               |         | 928 |

```

? APPLICANT: KALTENBOECK, BERNHARD
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
? TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
? TITLE OF INVENTION: CHLAMYDIA PSITTACI
? FILE REFERENCE: UTSD:659
? CURRENT APPLICATION NUMBER: US/09/738,269
? CURRENT FILING DATE: 2000-12-18
? NUMBER OF SEQ ID NOS: 61
? SOFTWARE: Patentin Ver. 2.1
? SEQ ID NO 57
? LENGTH: 926
? TYPE: PRT
? ORGANISM: Chlamydia psittaci
? US-09-738-269-57

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|    | Query Match           | 37.7%  | Score 1802;         | DB 3;      | Length 926; |
|----|-----------------------|--|---------------------|------------|-------------|
|    | Best Local Similarity | 40.8%  | Pred. No. 3,26-110; |            |             |
|    | Matches 385;          | Conservative 172;  | Mismatches 354;     | Indels 32; | Gaps 15;    |
| Qy | 1                     | MKTSIPWLVSVLA--FSCHLOSANEELSPDPSFNGNIDSGTTPKTSATT----        | ys                  | 54         |             |
| Db | 1                     | MRPELYKILISTLTLPISFFHSQLAHEVALTQESIIDAN---GAFPPQSTRTAGTITYN  |                     | 57         |             |
| Qy | 55                    | LTGDFVFEYEEGKGPLSDSCFKQTDMLTFLGNCHSLTFEGIDGTHAGAAASTTANKL    |                     | 114        |             |
| Db | 58                    | VESDISIVDYGQDTAALASSAFVQZADNLTFEGNNHSLSTINANKGAPAGINVTADKIL  |                     | 117        |             |
| Qy | 115                   | TFSGFSLISDPSPTVTVTGQGTLSAGGVNLENIRKLVAAGNFSTADGAIKAGSEFL     |                     | 174        |             |
| Db | 118                   | TLTDFSLISRECCSLLVNTGKGMKGGALINLANNASILPDQVYSANGAISCNAFL      |                     | 177        |             |
| Qy | 175                   | TGTSGDALFSNNSSSTKGAIAATTAGARIANNNTGVAPLSNIASTGCAIDEGSTIISN   |                     | 234        |             |
| Db | 178                   | TGSSKEISFTTNTSTAKKGALIAAGI AHLSDNQGTIRFSGNTAVNSGAVVSEASMTIAG |                     | 237        |             |
| Qy | 235                   | NKFLYFEGNAKTT----GCAICTYASGSELLISNNKTLIFASNAVETSGGAIAHAKL    |                     | 290        |             |
| Db | 238                   | NNHVAFNNAVSGSDCCGAIHSCSKTGSATLTTRIDRKVILFEENNTSAKGAITYDKL    |                     | 297        |             |
| Qy | 291                   | ALSSGCFTEFLRNNVSSATPKGAIASIDASGELSLSAETGNIITVPRNTLTGSGTDPEKR |                     | 350        |             |
| Db | 298                   | ILTSGGPTAFINNKVTHATPKGAIIGLANBECCLTAEHGITT- DNNLTAMTDONATIKR |                     | 356        |             |
| Qy | 351                   | NAINIGSNGKFTELRAAKNHTIIFYDPITSEGTSDVLKINNGSAGALNPYQGTILFSGE  |                     | 410        |             |
| Db | 357                   | NAINIEGNGKRVNLRAASGKTISFYDPIVEGNADLLTLINKAEGD--KTYNGRIITFSGE |                     | 414        |             |
| Qy | 411                   | TLTDELKVDNLKSSFTQPVLSGGKLLLOKGYTLBESTSSQEAISLLGMDSGTTLSTT    |                     | 470        |             |
| Db | 415                   | KLTGEOAAVADNLKTTFTOPTTLAAGELVLAISGVEKATVQTAGSILMDAGKTSAK     |                     | 474        |             |
| Qy | 471                   | AGSITINLGINVSLGLKQPVLSLTAKASNKVYVSGKLNLDIEGNLYESHMFSDQLF     |                     | 530        |             |
| Db | 475                   | TEDATLTNLAINPTLDDGKFAVVDVAAGKNVLSGAIIGVIDPGRKYENHKNDTLAL     |                     | 534        |             |
| Qy | 531                   | SLKTIYDADVDYTNVISLLIPVAEDPENSEYFGQGNVNMVTTDTATNTKEATA--TWT   |                     | 588        |             |
| Db | 535                   | GGIGLDSGGSV--TTTNVPISHVVAE--THYGVQGNVSWVMKDNNDPDKTQAIPTWNN   |                     | 590        |             |
| Qy | 589                   | KTGVPSPERKSALVCNTLMGVFDISLQQLVEIGATG-MEHKQGFVVSMTNPLHKTG     |                     | 647        |             |
| Db | 591                   | KTGVPNPERAPAPLVLSLWGSFTDLRSIQVLESVDSILETRGLVWSGIGNFFHQR      |                     | 650        |             |
| Qy | 648                   | D-EKRKGRRHSGGVIGGSAHTPDDLTFFAFCHLPARDDCFAHNNSRTYGGTLFFK      |                     | 706        |             |
| Db | 651                   | NAENRK-FRLHSSGVILGATTTNSTRBDSLVAFCOLPKAKDXLYVSKAANVYAGSVYQ   |                     | 709        |             |
| Qy | 707                   | HSHTLQOPONYLRLGRKAPSESAIEKFPREIPDALDVQVFSHSDNRMETHYTSLEDSGS  |                     | 766        |             |
| Db | 710                   | HVSKRPDDLTRLFNG----PNTCCGSFSKEIPIPLDAQITLYCHTANMTTSYTDPEVKS  |                     | 765        |             |
| Qy | 767                   | WSNECIAGIGLUDLF-VLSNPHLEKTFITQMKVENVYVSONSFESSSDGRGSGIRGL    |                     | 825        |             |



|     | Qy               | Dy  | Qy  | Dy | Qy | Dy |
|-----|------------------|---|-----|----|----|----|
| 766 | WGNPDIGLTLSTVDP  | IPVFSS--SIFDSVAPPAKLQVYVAHQDDFKEPTTEGRVFESSDL | 823 |    |    |    |
| 826 | LNLSIPVAGKVOGDI  | IGDSTYDLSGFPISDVYRNPNPOSTALTNMSPDWKRGUJLSRO   | 885 |    |    |    |
| 824 | LNVSVPFKIKTEKLSY | GERSAVDLTLMYIPDYRNPNPSCMTGLAINDSVMTTATNTLAKQ  | 883 |    |    |    |
| 886 | AFLLRGSNVYVNSCEL | FGHYAMELRGSSRNINVDVGTCLRF                     | 928 |    |    |    |
| 884 | AFIYAGNHIALTSG   | VEVMSQGFELRSSRNYNVDLGKAVF                     | 926 |    |    |    |

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RESULT 6
US-10-023-437-57
: Sequence 57, Application US/10023437
: Publication No. US20020183272A1
: GENERAL INFORMATION:
: APPLICANT: JOHNSTON, STEPHEN A.
: APPLICANT: STEMKE-HALE, KATHERINE
: APPLICANT: SYKES, KATHRYN F.
: APPLICANT: KALTENBOECK, BERNHARD
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACIDIC SEQUENCES OF CHLAMYDIA
: TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
: FILE REFERENCE: US/02,736US
: CURRENT APPLICATION NUMBER: US/10/023,437
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: 60/225,839
: PRIOR FILING DATE: 2000-12-15
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 57
: LENGTH: 926
: TYPE: PR1
: ORGANISM: Chlamydia psittaci
: US-10-023-437-57.

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|                       |                  |                    |           |            |
|-----------------------|------------------|--------------------|-----------|------------|
| Query Match           | 37.7%            | Score 1802         | DB 4      | Length 926 |
| Best Local Similarity | 40.8%            | Pred. No. 3.2e-110 |           |            |
| Matches 385           | Conservative 112 | Mismatches 354     | Indels 32 | Gaps 15    |

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Dh 475 TEBATLTNLAINPNTLDGKKFAVNDVAAGKNVTLSSALGVIDPTGKFEHKNLDTLAL 534
Qy 531 SLIKITVDADVNTNDISSLIPVPAEDPNSEYGFQGMNWNMTDTLATNTYKATA--TWT 588
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Dh 535 GGIGLSGKSV--TTTNVPSHVGAEE--THYGYQGNMVSVMVDKNNSDPXTQAIAPTN 590
Qy 589 KTGFVSPERKSAIYCNLTLMGVFTDIRSLQOLVEIGATG-MENHQGFVWSMTNFKLTG 647
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Dh 591 KTGYVNPERRAPLVLNLSMGSFIDLRISIQVLERSVDSILETRGLMWSGIGNPFHKDR 650
Qy 648 D-ENRKGFRHTGGYVIGGSATTPDDLTFTAFCHLPARDDCCTIANNSTYGTLPFK 706
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Dh 651 NAENRK-FRHISSGYVLGATNTSREDSLSVAFCOLFAKQDYLVSXKAAVAVAGSYYYQ 709
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Qy 707 HSTLTLPQVYLYLGRAPKSESAIEKFRPEIPLADVQVSPSHSNRKETHYLSLPEEGS 766
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Dh 710 HYSKFPDDLTRLFNG---PNTCCSGSFKEIPIFLDAQITTYCHTANNMTSTYDVPYKGS 755
Qy 767 WSNECIAGIGLDLPE-VLSNPHLPFKFIQIMQKVEWYVSONSFPESSSDGGRFSGRL 823
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Dh 766 WGNDTLGLTLSTSVLPVFFSS--SIFDSYAPAPAKIQVYAHQDDPKFPTTEGRVFEBSDL 822
Qy 826 LNIISIPVAKAFQOAGDIGDSYTYDLSGFVSDVYRNPNPOSTATLVMSPEMSKIRGNSLRQ 885
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Dh 824 LNVSVETIGIKFEKLSYGRSAYDLTLMTKIPDVYRHNSPCTGLAIINDVSMULTATNLARQ 883
Qy 886 AFLLRGSNNVYVNSNCELFCHYAMEALRGSSSRNVYVDVQTKLRF 928
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Dh 884 AFLVPRAGNHIALTSGVEMSPQGFELBRSSRNRYNDLCAKAPF 926

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RESULT 7
US-10-312-273-33
: Sequence 33. Application US/10312273
: Publication No. US20040005667A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
: TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
: FILE REFERENCE: P025035WO
: CURRENT APPLICATION NUMBER: US/10/312,273
CURRENT FILING DATE: 2002-12-20
: PRIOR APPLICATION NUMBER: 0016363.4
PRIOR FILING DATE: 2000-07-03
: PRIOR APPLICATION NUMBER: 0017047.2
PRIOR FILING DATE: 2000-07-11
: PRIOR APPLICATION NUMBER: 0017983.8
PRIOR FILING DATE: 2000-07-21
: PRIOR APPLICATION NUMBER: 0019368.0
PRIOR FILING DATE: 2000-08-07
: PRIOR APPLICATION NUMBER: 0020440.4
PRIOR FILING DATE: 2000-08-18
: PRIOR APPLICATION NUMBER: 0022583.9
PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 0027549.5
PRIOR FILING DATE: 2000-11-10
: PRIOR APPLICATION NUMBER: 003706.5
PRIOR FILING DATE: 2000-12-22
: NUMBER OF SEQ ID NOS: 664
: SOFTWARE: Seqw1n99, version 1.02
: SEQ ID NO 33
LENGTH: 928
: TYPE: PRT
: ORGANISM: Chlamydia pneumoniae
US-10-312-273-33

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Qy      1 MKTSLPVLVSSYLAFLSCHLQ---SLANEELLSPDDSEFNQINDSGFTF-----KTSAT   51
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Ob      1 MKSLLMPFLFISSLPLPLSLNFAAFAAVEINLGNTSFSG--PGYTTPAQTNNADGT   57
Matches 40%; Conservative 152; Mismatches 35; Indels 38; Gaps 17

```

QY 52 TYSITGADVFEYBPGKTPPLSDSCFKQTTDNLTLFLNGHSLTRFGIDAGTHAGAASTTAN 111  
 Db 58 IYVLTGDSITNAGSPITALTASCFKETTGNLSFGHGYQFLQNDIDAGANC-TFTWTAN 116  
 QY 112 KNLTFSGFSLSPSSPTVTTGGTLLSAGVNLNKRLLVAVNGFSTADGALIKGAS 171  
 Db 117 KLSFSGFSYLSL--IQTNNATTGTGAIKSTGACISQSNVSCYFGQNFSDNGALQGS 174  
 QY 172 FLITGTSGDGLFSNNSSSTGGAIAATAGARIANNVTGYRFLSNLSTAGAIIDEGTSI 231  
 Db 175 ISLS-LNPULTFAKNKATOKGALYSTGCTITNTNLASASEBTANNGALYTEASSF 233  
 QY 232 LSNKKFLYFEGN--AAKTGGAI-CNTKASGSEPLIISNNKTLIFASVAETSGAIIA 287  
 Db 234 ISSKKAISFINNSVTATSGATGALYCSTSPKPVLTLDNGELNFIQNTAITSGAIIY 293  
 QY 288 KKLALSSGGTFTEFLRNN-VSSATPKGALSIDASGELISAEFGNTTFVRNLTLT-TGST 345  
 Db 294 DNLVLSSGGPTLFFKNNSAIDTAAPLGAIALADSGSLSLALGDDITFEQNTVVKAGSS 353  
 QY 346 DTPKRNAINIG-SNGKFTEFLRAAKNHTIFFYDPTISGTS--SDVLKINNGSAGALNPYQ 402  
 Db 354 QTTNRNSINIGNNAIKVQLRASQNTIIFYDPTITSTIALSDALNLNGPDLAGNAPYQ 413  
 QY 403 GTILFSGETLTADELKVADNLKSSFTQPVLSGGKLLQKGVLTLESTFSQEAAGLLGMD 462  
 Db 414 GTIVSGEKLSEAAEADNLKSTIQOPLTLAGQLSLKSGVTLVAKSFQSPSTLLMD 473  
 QY 463 SGTTLSTTAGSITTTNLGINVDSLGLKOPVSLTKAGSNKVIYSGKLNLDIEGNTYESH 522  
 Db 474 AGTTLLETADG-ITINNVLAVNDSLKETKATLKATQASQVTLTSLVDSLVPSGNVYEDV 532  
 QY 523 MFSHDOLFSLKITVDADVDTNVDISLIIPVPAEDPNSEYGFQGNVNVMTTDAATNKE 582  
 Db 533 SWNPQVFSCLTIT--ADDPANIHITDLADPLEKPIHMGYGNALMSQEDTATKSKA 590  
 QY 583 ATATWTKTGFPVSPERKSALVNTLWGVFTDIRSLQOLVEIGATGMEHKQFVWSSMTNF 642  
 Db 591 ATLWTGTGVNPNBERGRTLVAANTLWGSFVDVRSIQOLVATKVRQSOETRGICEGISNF 650  
 QY 643 LHKGTDENRKGFRTSGGYIVGGSANRPKDLTFPAFCHLFADKOCFLAHNNSRTYGGT 702  
 Db 651 FHKOSTKINKGFRRHISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKNRSAVAAS 710  
 QY 703 LFFGHSHTLQPONYLRLGRAKFSESAIEKPREIPLALDVQVFSHSDNRMETHYLSLPE 762  
 Db 711 LHLQHLATLSSPSLIRY--LPSES-----EQPVLFDAQISYIYSKNTMKTYTQAPK 761  
 QY 763 SEGWSNCEIAGIGLDLPFVLNSNPHLPFKTFIPQMKVENVVYQNSFFESSD-GRFS 821  
 Db 762 GESSWYNDGALBELASLPHITALSHEGLFHAVPFPIKVEASYIHQDSFKERNTTLVRSFD 821  
 QY 822 IGRLLNLSIPVAKFVQGDIGDSTYTDLSGFFVSDVYRNNPQSTATLVMSDMSKIRGN 881  
 Db 822 SGDLINVSVPITGIFTERPSRNERASYEATVIYVADVVRKPNDCJTALLINNTSMKTTGTN 881  
 QY 882 LSRQAFILRGSNNTVYNSNCELFHYAMELGRSSNNTVADVGTKLRF 928  
 Db 882 LSRQAGIRAGIFYAFSPNLEVTYNSLMEIRKSSRSYADLGKRFQF 928

## RESULT 8

US-10-503-135-99  
 ; Sequence 99, Application US/10503135  
 ; Publication No. US20050152926A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BENSI Giuliano  
 ; APPLICANT: GRANDI Guido  
 ; TITLE OF INVENTION: CYTOTOXIC T-CELL EPITOPES FROM CHLAMYDIA  
 ; FILE REFERENCE: 002441.00089  
 ; CURRENT APPLICATION NUMBER: US/10/503,135  
 ; CURRENT FILING DATE: 2004-08-11  
 ; PRIOR APPLICATION NUMBER: PCT/IB03/01161

; PRIOR FILING DATE: 2003-02-13  
 ; PRIOR APPLICATION NUMBER: GB-0203403.1  
 ; PRIOR FILING DATE: 2002-03-13  
 ; NUMBER OF SEQ ID NOS: 181  
 ; SOFTWARE: SeqW199, version 1.02  
 ; SEQ ID NO 99  
 ; LENGTH: 928  
 ; TYPE: PRT  
 ; ORGANISM: Chlamydia pneumoniae  
 US-10-503-135-99

Query Match 37.5%; Score 1794; DB 5; Length 928;  
 Best Local Similarity 42.7%; Pred. No. 1.1e-109;  
 Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;

QY 1 MKTSPVNLVSVIAPSCHQ-----SIANEELSPDPSFNGNIDSGTFPP-----KTSAT 51  
 Db 1 MMSLHWFLISSLALPLNSAPAAVEINLGPINFSFG---POTYTPPQNTNADGT 57  
 QY 52 TYSITGADVFEYBPGKTPPLSDSCFKQTTDNLTLFLNGHSLTRFGIDAGTHAGAASTTAN 111  
 Db 58 IYVLTGDSITNAGSPITALTASCFKETTGNLSFGHGYQFLQNDIDAGANC-TFTWTAN 116  
 QY 112 KNLTFSGFSLSPSSPTVTTGGTLLSAGVNLNKRLLVAVNGFSTADGALIKGAS 171  
 Db 117 KLSFSGFSYLSL--IQTNNATTGTGAIKSTGACISQSNVSCYFGQNFSDNGALQGS 174  
 QY 172 FLITGTSGDGLFSNNSSSTGGAIAATAGARIANNVTGYRFLSNLSTAGAIIDEGTSI 231  
 Db 175 ISLS-LNPULTFAKNKATOKGALYSTGCTITNTNLASASEBTANNGALYTEASSF 233  
 QY 232 LSNKKFLYFEGN--AAKTGGAI-CNTKASGSEPLIISNNKTLIFASVAETSGAIIA 287  
 Db 234 ISSKKAISFINNSVTATSGATGALYCSTSPKPVLTLDNGELNFIQNTAITSGAIIY 293  
 QY 288 KKLALSSGGTFTEFLRNN-VSSATPKGALSIDASGELISAEFGNTTFVRNLTLT-TGST 345  
 Db 294 DNLVLSSGGPTLFFKNNSAIDTAAPLGAIALADSGSLSLALGDDITFEQNTVVKAGSS 353  
 QY 346 DTPKRNAINIG-SNGKFTEFLRAAKNHTIFFYDPTISGTS--SDVLKINNGSAGALNPYQ 402  
 Db 354 QTTNRNSINIGNNAIKVQLRASQNTIIFYDPTITSTIALSDALNLNGPDLAGNAPYQ 413  
 QY 403 GTILFSGETLTADELKVADNLKSSFTQPVLSGGKLLQKGVLTLESTFSQEAAGLLGMD 462  
 Db 414 GTIVSGEKLSEAAEADNLKSTIQOPLTLAGQLSLKSGVTLVAKSFQSPSTLLMD 473  
 QY 463 SGTTLSTTAGSITTTNLGINVDSLGLKOPVSLTKAGSNKVIYSGKLNLDIEGNTYESH 522  
 Db 474 AGTTLLETADG-ITINNVLAVNDSLKETKATLKATQASQVTLTSLVDSLVPSGNVYEDV 532  
 QY 523 MFSHDOLFSLKITVDADVDTNVDISLIIPVPAEDPNSEYGFQGNVNVMTTDAATNKE 582  
 Db 533 SWNPQVFSCLTIT--ADDPANIHITDLADPLEKPIHMGYGNALMSQEDTATKSKA 590  
 QY 583 ATATWTKTGFPVSPERKSALVNTLWGVFTDIRSLQOLVEIGATGMEHKQFVWSSMTNF 642  
 Db 591 ATLWTGTGVNPNBERGRTLVAANTLWGSFVDVRSIQOLVATKVRQSOETRGICEGISNF 650  
 QY 643 LHKGTDENRKGFRTSGGYIVGGSANRPKDLTFPAFCHLFADKOCFLAHNNSRTYGGT 702  
 Db 651 FHKOSTKINKGFRRHISAGYVVGATTTLASDNLITAAFCQLFGKDRDHFINKNRSAVAAS 710  
 QY 703 LFFGHSHTLQPONYLRLGRAKFSESAIEKPREIPLALDVQVFSHSDNRMETHYLSLPE 762  
 Db 711 LHLQHLATLSSPSLIRY--LPSES-----EQPVLFDAQISYIYSKNTMKTYTQAPK 761  
 QY 763 SEGWSNCEIAGIGLDLPFVLNSNPHLPFKTFIPQMKVENVVYQNSFFESSD-GRFS 821  
 Db 762 GESSWYNDGALBELASLPHITALSHEGLFHAVPFPIKVEASYIHQDSFKERNTTLVRSFD 821  
 QY 822 IGRLLNLSIPVAKFVQGDIGDSTYTDLSGFFVSDVYRNNPQSTATLVMSDMSKIRGN 881

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Db      822 SGDLINVSPIGITEFRPERSNERASYSATYIYADVRYRKNPDCCTALLINNTSKTGTIN 881
Qy      882 LSRQAFLLRGSNNVYNSNCELFGHYAMELRGSSRNYNVDVGTLRP 928
      882 LSRQAGIGRAGIFYAFSPNLEVTNLSMEIRGSSRSRYNADLGKQFQ 928

RESULT 9
US-10-312-273-95
; Sequence 95, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; PRIOR APPLICATION NUMBER: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 95
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-95

Query Match      37.3%; Score 1784; DB 4; Length 928;
Best Local Similarity 40.4%; Pred. No. 5e-109;
Matches 385; Conservative 174; Mismatches 343; Indels 52; Gaps 18;

Qy      1 MKTSIPWVYVSSVYA--FSGHLOSANBELSPDSDNGNIDSGTFPPKTSAT--TYSLT 56
Db      1 MKQFSLVLSSTLACTSCSTVPAATAENIGPDSDFGSTNGTYTPKNVTTGIDYTLT 60
Qy      57 GDVFFYEPGKGTPLSDSCFKQTTDNITFLGNHSLTFGFTIDAGTHAGAASTTANKULTF 116
Db      61 GDTILQNLGSAALTKCFSDITTESLSFAGKGYSLSLNKKSAE--GAALSVTTDKNLSL 119
Qy      117 SGFSLSDSSPSTVTT--GQGTLSAGAGVNLNIRKLVVAGNFSTADGAIKGSFLL 174
Db      120 TGFSSLTFLAPASVITTPSGKAVKCGDLTFDNNGTILFKQDYCEHNGAISTKNLSL 179
Qy      175 TGTSGDALFSGNNSST--KGAIAITTAGARIANNITGYVFLSNIASTSGAIDDEGTST 231
Db      180 KNSGTGISFEGNKSASATGKGAICATGTVDITNNATPLFSNNIAEAGGAINSTGNCCT 239
Qy      232 LSNKKFLYFEGNAKKT--GGAICNTKASGSPELLISNNKTLLIFASNVASTSGAIIHAK 288
Db      240 ITGNTSLVFSENSVTATAGNGAL-----SGDADVTISNGSVTFSGNQAVANGAIYAK 294
Qy      289 KLAIS--GGFTBELNNVSSATP-KGAISIDASGELSLAETGNTTFVRNTLTJTTGST 345
Db      295 KLTILASGGGVSPPLITIIYOGTTAGNGAISIILAGCESLSABAAGDITFGNAIVAT-TP 353
Qy      346 DTPEKRNINIGSNCKFTLELAAKNHTIFFYDPTTSE--GTSSDVLKTNNSAAGALNPYG 403
Db      354 QTTKRNSIDIGSTAKTINLRAISGHSIFFYDPTTANTAADSTDTJLNLNKAAGNSTDYSG 413
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Qy      404 TILFSGETITADELKYADNLIKSPFTQPSLGGKLLQKGVLTLESTSFQEGAGSLIGMS 463
Db      414 SIYFSGEKLSDEBAKVADNLTSLKQPVTLTGNVLTKXGVLTLDTGFGTQAGASSYIMA 473
Qy      464 GTTLSTTAGSIITTNLGINVDSIGLKQPVSLTKAGSANKYIVSGKLNLDIBENITESM 523
Db      474 GTTLKASTEBVTLTGISIPVDSLGBGKAVIAASAASKVVALSLGPIILLDNOGNAENHD 533
Qy      524 FSHDQFLSLKTVADVDVNTNDISSLIPVPAEDPSEYEGFOGQNNVMTTDPAT--NPK 581
Db      534 LKGTQDFSVQJSA-LGTAITTTDVPA--VPVYATPTHYGYQGTMGATWDDTASTPRTK 589
Qy      582 EATATWTKTGFVSPERKSAVLCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTN 641
Db      590 TATLAATNTGYLPNPERQCPVLVNSLWGSFSDIQAIQVILRSALTLCSDRGFWAGVAN 649
Qy      642 FLHKTDENRKGRHRTSGGVVIGSAAHTRKDQLFTAFCHLPARDQCTIAHNSSTYGG 701
Db      650 FLDKDKKGRKRYKRRHSGGYAIGGAQTCSENLISPAFQULFGSDKDFLVAKNHTTYAG 709
Qy      702 TLFFKSHTLQPNVYRLGRAKFSESAIKFP--REIPLADQVSPFSDNRMETHYT 758
Db      710 AFYIQHTEC-----SGFIGCLDLKLPQSMHKEFLVBEGQLAYSHVSHDLTKYTT 759
Qy      759 SLPESEGSNSNECIAGIGLDLPFVLSNHP--LEKTFIDPMKVEYVYVSGNSPFESS 814
Db      760 AYPEVAGSWGNNAPFNNMLAS-----SHSYPEYLHCFDTPYAPYIKNLTYIRQDSFEKG 814
Qy      815 SDGRGFSIGRLNLSIPVAKFVQGDIGSYTYDLSGFPVSDVYRNPNOSTATLVNSPDS 874
Db      815 TEGRSFDDSNLFTNLSPIVKEKFEKFCDCNDFSYDLTLSTVPPDLIRNDPKCTTALVIGAS 874
Qy      875 WKIRGNLSROAFLIRGNNVYNSNCELFGHYAMELRGSSRNYNVDVGTLRP 928
Db      875 WETYNANLARQALQVAGSHYAFSPWFVVLGQFVEVRGSSRYNVDLGKQFQ 928

RESULT 10
US-10-289-762-470
; Sequence 470, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-470

Query Match      36.9%; Score 1763; DB 4; Length 930;
Best Local Similarity 41.7%; Pred. No. 1.2e-107;
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

Qy      1 MKTSIPWVYVSSVYVSSCHLOSAN---BELSPDSDFGNIDSGTFPPKTSAT---TTY 53
Db      1 MKIPLKLLISSITLVPI-LLSIATYGADASLSPDSDFG-AGSFTFKSTADANGTY 58
Qy      54 SLTGDVFFYEPGKGTPLSDSCFKQTTDNITFLGNHSLTFGFTIDAGTHAGAASTTANKN 113
Db      59 VLSGNYIINDACKGTALTCCEFTETTGDLTFGKGYSFSGFNIVVDAGSNAGAASTTADKA 118
Qy      114 LTFSGFSLSDSSPSTVTTTGGTLLSAGGVNLNIRKLVVAGNFSTA--DGAIKGA 170
Db      119 LFTFGSNLSFTIAPAPETIYASGKSTLSAGALNLTGNTILTSQVNSPANNNGGAIYAK 178
Qy      171 SFLLTGTSGDALFSGNNSSTKGAIAITTAGARIANNITGYVFLSNIASTSGAIDDEGTST 230
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|    |     |  |     |
|----|-----|--|-----|
| Db | 179 | TLISIGNTSSITTTSSAKKGLGALISSAASISGNTQOLVFMNNKGETGGALGFPAAS        | 238 |
| Qy | 231 | ILSNKFLYFEGNAAKTT--GGALCNTYASGSPELLISNNKTLIFASNAVETSGGAIHA       | 287 |
| Db | 239 | SITQNSSLFFSGGWTATDADAGKAGALICEYKGTGETPLTITSGAKSLTFPEMNSVTOGGALCA | 298 |
| Qy | 288 | KXIALSSGGETPELRNV--SSATPRYGASISIDASELSLMECNIPVNNTLTTGSTD         | 346 |
| Db | 299 | HGDLSSAAGTTFESNNRCNTAAGGALALDSSLSLSMNOGDTITLGGTLTST-SAP          | 357 |
| Qy | 347 | TPKRNAINIGSNKFEFLPAKKNHTTFEYDPTISEGT--SSDVLKINNGSAGALNPYOGTI     | 405 |
| Db | 358 | TSIRNMALYGGSAKINLRAAQGGSIYFPDPIASNTTASDVLITNQDPDSPLDYGTLI        | 417 |
| Qy | 406 | LFSGETLTADLKVADNLKSFQPVSLSGGKLLIQKVTLESTFSFOEAGSLIGDSCGT         | 465 |
| Db | 418 | VFSGEKLSADEEAQAADNFTSILKOPALASGTLAKGNVELDVNGFTQTEGSTLLMQPGT      | 477 |
| Qy | 466 | TLSTTAGSITTNGLIVNDSLGKOPVSLTAKGASNKIVYSGKLNLDIBENIYESHMF5        | 525 |
| Db | 478 | KLKAADTEALISLTLYVDLSALBEGNSVSLETGANKAKTTITLSPLYFQDSSNPFESHTI-    | 536 |
| Qy | 526 | HDQLFSL-LKTIYDADVDNTVDISLIPVADBPNSSEYFOGQNNVMNTTDTATNTKEAT       | 584 |
| Db | 537 | -NQAFQPLVPLVPAATAASDIYIDALLTSPVQTPPEPHYGQGHBEATW-ADTST-AKSGT     | 593 |
| Qy | 585 | ATWTKGFVPSPERKALVCNTLMGVTDIRLSLOQVLEIGATGMEHOGFVVSMTNFEH         | 644 |
| Db | 594 | MTWTTGGVNNPERRRASVVPDLSMASFTDIRLQOIMTSQANSIYQOKGLASTANAFPH       | 653 |
| Qy | 645 | KTGDNKRGFRHTSGGVIGVSGASMTPEKODLFTFAECHTFARDKOCFIANNRSRYGGTLF     | 704 |
| Db | 654 | KDKSGTQOAPRHKSXYGIYVGSADBPSENIPEVARCOQLFKDKDLFIYENTSHNYLASY      | 713 |
| Qy | 705 | FKSHTLTQPONYRLRGAKFSSSALEKPREIRPLALDVQVSFHSISDNRMETHYISLPESE     | 764 |
| Db | 714 | LOHRAFLG-----GLPMPSPFOSITDMUKDPLILMQLSISYTKMDMDRRYSYSEAQ         | 766 |
| Qy | 765 | GSMNNECTAGGIGLDLPVLYSNPHLPFKTFIQMKVEMVWYVYSSONSFPFESSDGGFSGIR    | 824 |
| Db | 767 | GSMWNSGALDELGGSLALYLPKAPFPQGYFFPLFLFOAVYISROQNFKESGAEARAFDDGD    | 826 |
| Qy | 825 | LNLNLSIPVGAQFYOGDIDGSIYTYDLEGFVSDVYRNNQSTATLVMSPDSWKIRGNLSR      | 884 |
| Db | 827 | LVNCISIPVGRLEKISDEKNNPEISLAYIGVYRKRNPSRITSLWVSASWTSJCKMLAR       | 886 |
| Qy | 885 | QAFILRSNNVYVNSNCELFQGHAMELBRSSNNVNDVGTKLRF                       | 928 |
| Db | 887 | QAFILASAGSHLTLSPHVELSGEAAVYELRRSAHIVYNDGCLARSF                   | 930 |

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, RESULT 11
, US-10-312-273-45
, Sequence 45, Application US/10312273
, Publication No. US20040005667A1
, GENERAL INFORMATION:
, APPLICANT: CHIRON SPA
, TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
, FILE REFERENCE: P025035WO
, CURRENT APPLICATION NUMBER: US/10/312,273
, CURRENT FILING DATE: 2002-12-20
, PRIOR APPLICATION NUMBER: 0016363.4
, PRIOR FILING DATE: 2000-07-03
, PRIOR APPLICATION NUMBER: 001047.2
, PRIOR FILING DATE: 2000-07-11
, PRIOR APPLICATION NUMBER: 001983.8
, PRIOR FILING DATE: 2000-07-21
, PRIOR APPLICATION NUMBER: 0019368.0
, PRIOR FILING DATE: 2000-08-07
, PRIOR APPLICATION NUMBER: 0020440.4
, PRIOR FILING DATE: 2000-08-18
, PRIOR APPLICATION NUMBER: 0022583.9
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; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 45
; LENGTH: 930
; TYPE: prt
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-45

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|                       |                   |                     |            |             |
|-----------------------|-------------------|---------------------|------------|-------------|
| Query Match           | 36.8%;            | Score 1761;         | DB 4;      | Length 930; |
| Best Local Similarity | 41.7%;            | Pred. No. 1.7e-107; |            |             |
| Matches 394;          | Conservative 165; | Mismatches 355;     | Indels 30; | Gaps 14;    |

[illegible]



NAME/KEY: SITE  
LOCATION: 1...927  
OTHER INFORMATION: Xaa=unknown or other  
US-10-289-762-472

Query Match 36.8%; Score 1758.5; DB 4; Length 927;  
Best Local Similarity 42.0%; Pred. No. 2,4e-107;  
Matches 398; Conservative 153; Mismatches 357; Indels 39; Gaps 17;

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QY 1 MKTSLPVLVSVYAFSGCHLO----SLANEHLLSPDDSPFNGNIDSGTFP-----TKSAT 51
DB 1 MKSSLHMFLLSSSLALPLSLNFSAPAAVAVENLNPINSFSS---PGYTPPAQTTNADGT 57
QY 52 TYSLTGVFEYEPKGPFLSDSCFKQTTDNLTLFGNGHSLTFEFGIDAGTHAGAASTTAN 111
DB 58 IYNLTGVSTINNASPTALTLASCKRETTGNLSFGHGQFLQIINDAGANC-TFTNTPAN 116
QY 112 KNLTFSGFSLSPDSSPSTVTGQTLSSAGVNLNIRKLVVAGNFSTADGAIKAS 171
DB 117 KLSFSGFSYSLT--IOTTNATGTGAIKSTGACSIQSNVSCYFGQNFSDNGALQSSS 174
QY 172 FLTLGTSGDALFSSNNSSTKGAIATTAGARIANTGVYRFLSNASTSGAIDEGTSI 231
DB 175 ISLS-LNPNLTFAPKNKATQKQALYSTGCTINNTLNASFSFSEMTAANNGAIYTEASSF 233
QY 232 LSNKKFLYFEGN---AAKTGGAICNTKASGPELIISSNKKTLIFASNVAETSGAIIHA 287
DB 234 ISSKKAISFINNSVTATGATGAIYCSSTSAKPVLTISDNGELNFTGNTAITSGAIIYT 293
QY 288 KKLALISGGTFEPLRN--VSSATPKGAISIDASGELSLSAETGNITFVNTLT--TGST 345
DB 294 DNLVSSGSGPTLFFKNNSAIDTPAAPGGAIAIADSGSLSLSALGDIETREGNTVVKGASS 353
QY 346 DTPRNAINIG-SNCKFTELRAAKNHTFEYDPTISEGTS--SDVLKINNSAGALNPYQ 402
DB 354 QTTTNSININNTAKIVQLPASQGNITFYDPTITSITLALSDNLNNGPDLGNPAPYQ 413
QY 403 GTILFSGEITLPADELKVADNLKSFPTQVSLSGKLLIQKQVLESTSFQSOEAGSLIGMD 462
DB 414 GTIYFSGEKLSEBAEAHADNLKSTIQOBLTLAGGLSLKSGVTIIVAKSFGSPSTLIMD 473
QY 463 SGTITSTAGSITTTNLGINVDSIGLKQPVSLTAKGASNKVIYSGKLNLDIEGNIYESH 522
DB 474 AGTTLLETADGSLSI--ICSQCFELKRDQEXTLKATQAQOTTLTSGSLSLVLPPSGVVEDV 531
QY 523 MFSHQLSLKITADADVDTNVDISLIPVAPEDPNSEYGFQOGOMNVMTTDTATNKE 582
DB 532 SMNNOVFSCLTLT--ADDPANIHITDLADPLEKNPIHWGVOGNWALSMQEDTRATSKA 589
QY 583 ATATWTKTGFVPSPERKSAIVCNTLMGVFTDIRSLQOLVEIGATGMEHKQFVWVSMTNF 642
DB 590 ATLWTTKGVNPNPERRGTLVANTLMGSPVDVRSIQOLVANKVRSQSTRIGIWECEGISNF 649
QY 643 LHKGTDENRKGFRHTSGGVIGGSAHTPKDILFTFAFCHLPARDKCTIAHNSRTYCGT 702
DB 650 FHKDSTINKGPRHSAGVVGATTTLASDNLITAAFCQLFQKDDHFINNKRASAYAAAS 709
QY 703 LFFKSHLQPNVYRLGRAKSESAIKFPRREIPLADVOVSPFHSNRMETHTYLSPE 762
DB 710 LHLQHLATLSPSLRY--LPGSES-----EQVLPDAQISYVSKNMTKTYTQAPK 760
QY 763 SEGSSNECIAAGIGLDLPVLSNPHPLFKTFIPOMKEMVNVSONSPRESSD--GRFSS 821
DB 761 GESSYNDGCALELASLPHTLASHEGLFHAFFIKYEBASTIHODSKRENTTLIVRFD 820
QY 822 IGRLLNLSPVGAKEVQGDIGDSYTYDLSGFFVSDVYRNNPOSTALTLVMSPDMSKIRGN 881
DB 821 SGDLINAVSPICITFERESRNERASYEAFVIYVADVRYRNPDCETALLINNTSMKTGTN 880
QY 882 LSRQAFLLRGSNNYVNSCELFQHYAMELRSSSNVNVDTKLF 928
DB 881 LSRQAGIRAGIIFYAFSPMLEVTNLSMEIRSSRSYNADLGKQPF 927

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RESULT 14  
US-09-452-380-3  
Sequence 3, Application US/09452380  
Patent No. US20020094340A1  
GENERAL INFORMATION:  
APPLICANT: WORDIN, Andrew D.  
APPLICANT: WOMEN, Raymond P.  
APPLICANT: WANG, Joe  
APPLICANT: DUNN, Pamela  
TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND  
TITLE OF INVENTION: US5 THEROP  
FILE REFERENCE: 032931/0216  
CURRENT APPLICATION NUMBER: US/09/452,380  
CURRENT FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: US 60/132,272  
PRIOR FILING DATE: 1999-05-03  
PRIOR APPLICATION NUMBER: US 60/113,439  
PRIOR FILING DATE: 1998-12-01  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3  
LENGTH: 936  
TYPE: PRT  
ORGANISM: Chlamydia pneumoniae  
US-09-452-380-3

Query Match 36.3%; Score 1734; DB 3; Length 936;  
Best Local Similarity 39.3%; Pred. No. 1e-105;  
Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

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DB 1 MKSSVSLFSSSLPLFSLSLIVAAEVLTLDSNNNSYDGS--NGTTFVFTSTDAAGTYSL 59
QY 56 TGVDFYEPK--GTPLSDSCKQTTDNLTLFGNGHSLTFEFGIDAGTHAGAASTT--ANKN 113
DB 60 LSDVSPFNAGALAIPLASGCFLEAGDUTFGQOHAKFPAFINAGSAGVASTAADKN 119
QY 114 LTFSGFSLSPDSSPSTVT--TGQGLTSSAGVNLNIRKLVVAGNFSTADGAIKASAF 172
DB 120 LRPDFSRLLIISCPILLSPTQCALKSVGNLSLGNOSIITITQNPSSNGGVINTKNF 179
QY 173 LTLGTSGDALFSSNNSST--KGAIAITTAGARIANTGVYRFLSNASTSGAIIDEGTS 230
DB 180 LLSGTSQFASFSRNQAFTHGQGVVATGTITLNSPGIVSFGONLAKSGGALYSTDNC 239
QY 231 ILSNKKFLYFEGN---AAKTGGAICNTKASGPELIISSNKKTLIFASNVAETSGAIIH 286
DB 240 SITDNFQVIFDGNSSAMBAQAQGAICCTTTDKT--VTLGNKNLSFTNTNLTALTYGAIS 297
QY 287 AKKLALISGGTFEPLRNNSATP---KGAISIDASGELSLSAETGNITFVNTLTITTTG 343
DB 298 GLKVISAGGPTLF--QSNISGSSAGOGGGAIIINASGELALHATSQDITF--NNQVING 355
QY 344 STDTPKRNAINIGNGFTELRAAKNHTFEYDPTISEGT--SSDVLKINNSAGALNPY 401
DB 356 STSR--RNAINIIDTAKVTSIRAAATGSIYFYDPTINPGRAASTDLNLMADANSEIEY 413
QY 402 QGTLFSGEITLPADELKVADNLKSFPTQVSLSGKLLIQKQVLESTSFQSOEAGSLIGM 461
DB 414 GGAIVFSGEKLSPTEKAIANVSTIRQPAVLARGDVLVDGVTVPFKDLTQSPGSLIM 473
QY 462 DSGTTLSTTGSITITNLGINVDSIGLKQPVSLTAKGASNKVIYSGKLNLDIEGNIYES 521
DB 474 DGGTTLISAKENANSLNGLAVNLSLDGTNKAALTEAAADKISLSGTIALIDTBSRYEN 533
QY 522 HMFSDQLFSLKITVDADVDTNVDISLIPVAPEDPNSEYGFQOGOMNVMTTDTATNTK 581
DB 534 HNLKASATYPLLETLT--AGANGTITLALSTLTQEBETHYGVGNQOLSWA--NATSSK 590
QY 582 EATLTWTKTGVPSPERKSAIVCNTLMGVFTDIRSLQOLVEIGATGMEHKQFVWVSMTN 641

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Db 591 IGSINMTRGYIBSPERKSNLPLNSLWGNFIDIRISNOLLETYSGSGEPFERELMLSGIAN 650  
 Qy 642 FLKKTGDNKRGPRHTSGGYVIGSAAHTPKDLETPAFCHLPARDKOCFLAHNNSRTYGG 701  
 Db 651 FFYRDSMPFRHGRHISGAYALGTTATTPABDQITPAFCQLPARDNRHITGKHGDTYGA 710  
 Qy 702 TLEFKHSHTL-OPONYLRIGRAKFSESAIEKPREBIPALDVQVSFSDNRMETHYSL 760  
 Db 711 SLVFHHTEGFLDIANFL-WGKATRAPWVLSEISQIILPSFDAKFSYLHTDNHMKTYTDM 769  
 Qy 761 PSEBGSNSNECIAAGIGLDLPFLVLSNPHLPKFTIPQMKVBMVYVQNSFFESSSDGRGF 820  
 Db 770 SIIRGSRNDAPFACADIGASLPFVTSVPY-LIKEVEBFPVKQYIYAHQODFYERHAAGRAF 828  
 Qy 821 SIGRLNLSIPVGAKEFVGDIIGDSYTYDLSGPFVSDVYRNNPOSTATLWMSPDWKRIRG 880  
 Db 829 NKSSELINVELPIGTFPERDSKSEKGYDILTMVILDAIRNPKQCQISLIASDANMAAYGT 888  
 Qy 881 NLSRQAFLLRGSNNVYVNSNCELFGHYAMELRGSSRNVDVGTCLRF 928  
 Db 889 NLSRQGSVRAANHFQVNPHEIFGQFAFEVRSSSRNVTNLGSKCF 936

RESULT 15  
 US-10-324-129-3  
 ; Sequence 3, Application US/10324129  
 ; Publication No. US20030157124A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mordin et al.  
 ; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there  
 ; FILE REFERENCE: 77813-4  
 ; CURRENT APPLICATION NUMBER: US/10/324,129  
 ; PRIOR FILING DATE: 2002-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/113,439  
 ; PRIOR FILING DATE: 1998-12-01  
 ; PRIOR APPLICATION NUMBER: US 60/132,272  
 ; NUMBER OF SEQ. ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ. ID NO 3  
 ; LENGTH: 936  
 ; TYPE: PRT  
 ; ORGANISM: Chlamydia pneumoniae  
 ; US-10-324-129-3

Query Match 36.3%; Score 1734; DB 4; Length 936;  
 Best Local Similarity 39.9%; Pred. No. 1e-105;  
 Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

Qy 1 MKTSPVVLVSVYLAFCCHLQSLANBELSPDSEFNINIDSGTF-----TPKTSATTYSL 55  
 Db 1 MKSSVSWLFFSSSIDPLFSLSIVAEEVLDDSSNNSYDGS-NGTTFVYSTTDDAAGTYSL 59  
 Qy 56 TGDVFFVEPEK-GTPISDSCFKQTTDNLTFLGNGHSLTFGFIDAGTHAGAASTT-ANKN 113  
 Db 60 LSDVVSFQNAAGALGIPLASGCFLEKGGDLTFQGNQHALKFAPINAGSSAGTVAASTADKN 119  
 Qy 114 LTFSGFELLSFDDSPSTTVV-TGQGLTSSAGVNLLENIRKLVAAGNSTADGAIKASFP 172  
 Db 120 LTRFDFERLITICPSLLSLSPGQCALKSVGNLSLTGNSQIIFTONFSSDNGKINTKNF 179  
 Qy 173 LITGTSGDALFSSNNSSTT-KGGAIAATTAARIANNTGYRFLSNIASTSGAIDDEGTS 230  
 Db 180 LLSGTSQFASFSNQATGKGQGVVATGTTIENSFGIYVSFSONLAKSGGALYSTDNC 239  
 Qy 231 ILSNNKFLYFEGN---AAKTTGAICTNTYASGSPELIISNNKTLIFASVVAETSGAII 286  
 Db 240 SITDNFQVIFDQNSAMEAAQAGGAICTTDTK--VTLGNKVLSEFTNTALTYYGGAIS 297  
 Qy 287 AKKLAISGGTETELRNNVSATP---KGGAISIDAGSELISAEONITFVVRNTLTTTG 343  
 Db 298 GLKVSISAGPPTLF-QSNISGSSAGGCGGAINIASAGELALSATSGDITF-NNNOVTNG 355

Qy 344 STDTPKRNAINIGSNGKFTELRAAKNHTIFFYDPTISEGT--SSDVLKINNGSAGALNPP 401  
 Db 356 STST--RNAINIIDTAKTISIRAAQGSIFYVDPIINPGTAASDTLTNLNLDANSEIEY 413  
 Qy 402 QGTILFSGETLRDELKADNLSKSTFOVSLSGGULLQKGYTLESTESFSQAGLLGM 461  
 Db 414 GGAIVSGEKLSTFEKAIANVTSTIRQPAVLARGDLVLRDGTVTFKDLTQSPGSRILM 473  
 Qy 462 DSGTSTTAGAGTTTNNLGINVDSLGLKQPVSTAKGASNKVIVSGKLNLIIDEGNIYES 521  
 Db 474 DSGTTLASAKENLISGLVANNLSLSDGTAKKALKTAAADKNISLSSTIALIDEGSFYEN 533  
 Qy 522 HMEHSDQLSLKITVDADVDTNVDISLLIPVPAEDPNSGEYGGQGVNVMWTTDTAINTK 581  
 Db 534 HNLKASATYPLLELT--AGANGTITLGALSTLTLAGPETHYGYQGMQLSMA--NATSSK 590  
 Qy 582 EAAATYTKGFVPSPERKALVNTIAGVFTDIRSQOLVEIGATGMEHKQGFVWSMTN 641  
 Db 591 IGSINMTRGYIBSPERKSNLPLNSLWGNFIDIRISNOLLETYSGSGEPFERELMLSGIAN 650  
 Qy 642 FLKKTGDNKRGPRHTSGGYVIGSAAHTPKDLETPAFCHLPARDKOCFLAHNNSRTYGG 701  
 Db 651 FFYRDSMPFRHGRHISGAYALGTTATTPABDQITPAFCQLPARDNRHITGKHGDTYGA 710  
 Qy 702 TLEFKHSHTL-OPONYLRIGRAKFSESAIEKPREBIPALDVQVSFSDNRMETHYSL 760  
 Db 711 SLVFHHTEGFLDIANFL-WGKATRAPWVLSEISQIILPSFDAKFSYLHTDNHMKTYTDM 769  
 Qy 761 PSEBGSNSNECIAAGIGLDLPFLVLSNPHLPKFTIPQMKVBMVYVQNSFFESSSDGRGF 820  
 Db 770 SIIRGSRNDAPFACADIGASLPFVTSVPY-LIKEVEBFPVKQYIYAHQODFYERHAAGRAF 828  
 Qy 821 SIGRLNLSIPVGAKEFVGDIIGDSYTYDLSGPFVSDVYRNNPOSTATLWMSPDWKRIRG 880  
 Db 829 NKSSELINVELPIGTFPERDSKSEKGYDILTMVILDAIRNPKQCQISLIASDANMAAYGT 888  
 Qy 881 NLSRQAFLLRGSNNVYVNSNCELFGHYAMELRGSSRNVDVGTCLRF 928  
 Db 889 NLSRQGSVRAANHFQVNPHEIFGQFAFEVRSSSRNVTNLGSKCF 936

Search completed: November 25, 2005, 14:29:58  
 Job time : 101.698 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 14:03:16 ; Search time 28.7195 Seconds  
(without alignments)  
2671.458 Million cell updates/sec

Title: US-09-446-677b-2

Perfect score: 4782  
Sequence: 1 MTSIPWLVSSVLAFLSCHL.....MELRGSSRNVDVGTGLRF 928

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5.COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/6.COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/H.COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS.COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/RE.COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description                             |
|------------|--------|-------------|--------|-------|---|
| 1          | 4782   | 100.0       | 967    | 2     | US-09-438-185A-453<br>Sequence 453, App |
| 2          | 4774   | 99.8        | 949    | 2     | US-09-198-452A-478<br>Sequence 478, App |
| 3          | 1855   | 38.8        | 928    | 2     | US-09-428-122-2<br>Sequence 2, Appl     |
| 4          | 1794   | 37.5        | 937    | 2     | US-09-438-185A-449<br>Sequence 449, App |
| 5          | 1763   | 36.9        | 930    | 2     | US-09-198-452A-470<br>Sequence 470, App |
| 6          | 1761   | 36.8        | 938    | 2     | US-09-438-185A-448<br>Sequence 448, App |
| 7          | 1758.5 | 36.3        | 927    | 2     | US-09-198-452A-472<br>Sequence 472, App |
| 8          | 1734   | 36.3        | 947    | 2     | US-09-438-185A-447<br>Sequence 447, App |
| 9          | 1593   | 33.3        | 780    | 2     | US-09-438-185A-17<br>Sequence 17, Appl  |
| 10         | 1435.5 | 30.0        | 866    | 2     | US-09-438-185A-15<br>Sequence 15, Appl  |
| 11         | 1355   | 28.3        | 932    | 2     | US-09-438-185A-6<br>Sequence 6, Appl    |
| 12         | 1345   | 28.1        | 922    | 2     | US-09-198-452A-15<br>Sequence 15, App   |
| 13         | 1286   | 26.9        | 634    | 2     | US-09-438-185A-451<br>Sequence 451, App |
| 14         | 1286   | 26.9        | 643    | 2     | US-09-198-452A-474<br>Sequence 474, App |
| 15         | 1284.5 | 26.9        | 999    | 2     | US-09-438-185A-455<br>Sequence 455, App |
| 16         | 1278.5 | 26.7        | 973    | 2     | US-09-430-723-2<br>Sequence 2, Appl     |
| 17         | 1144.5 | 23.9        | 1414   | 2     | US-09-438-185A-446<br>Sequence 446, App |
| 18         | 1132.5 | 23.7        | 557    | 2     | US-09-198-452A-29<br>Sequence 29, App   |
| 19         | 1130.5 | 23.6        | 671    | 2     | US-09-198-452A-468<br>Sequence 468, App |
| 20         | 1125.5 | 23.5        | 602    | 2     | US-09-438-185A-18<br>Sequence 18, Appl  |
| 21         | 1092.5 | 22.8        | 1013   | 2     | US-09-612-402B-15<br>Sequence 15, Appl  |
| 22         | 1092.5 | 22.8        | 1013   | 2     | US-09-542-520-15<br>Sequence 15, Appl   |
| 23         | 1090   | 22.8        | 1012   | 2     | US-09-612-402B-2<br>Sequence 2, Appl    |
| 24         | 1090   | 22.8        | 1012   | 2     | US-09-542-520-2<br>Sequence 2, Appl     |
| 25         | 1089.5 | 22.8        | 1013   | 2     | US-09-612-402B-16<br>Sequence 16, Appl  |
| 26         | 1089.5 | 22.8        | 1013   | 2     | US-09-542-520-16<br>Sequence 16, Appl   |
| 27         | 1084.5 | 22.7        | 1006   | 2     | US-09-556-877-190<br>Sequence 190, App  |

|    |        |      |      |   |   |
|----|--------|------|------|---|---|
| 28 | 1084.5 | 22.7 | 1006 | 2 | US-09-620-412C-190<br>Sequence 190, App |
| 29 | 1084.5 | 22.7 | 1006 | 2 | US-09-598-419-190<br>Sequence 190, App  |
| 30 | 1071   | 22.4 | 984  | 2 | US-09-612-402B-43<br>Sequence 43, Appl  |
| 31 | 1069.5 | 22.4 | 982  | 2 | US-09-556-877-176<br>Sequence 176, App  |
| 32 | 1069.5 | 22.4 | 982  | 2 | US-09-620-412C-176<br>Sequence 176, App |
| 33 | 1069.5 | 22.4 | 982  | 2 | US-09-598-419-176<br>Sequence 176, App  |
| 34 | 1015.5 | 21.2 | 1132 | 2 | US-09-198-452A-466<br>Sequence 466, App |
| 35 | 995    | 20.8 | 507  | 2 | US-09-198-452A-32<br>Sequence 32, Appl  |
| 36 | 850    | 17.8 | 880  | 2 | US-09-556-877-175<br>Sequence 175, App  |
| 37 | 850    | 17.8 | 880  | 2 | US-09-620-412C-175<br>Sequence 175, App |
| 38 | 850    | 17.8 | 880  | 2 | US-09-598-419-175<br>Sequence 175, App  |
| 39 | 843.5  | 17.6 | 494  | 2 | US-09-198-452A-33<br>Sequence 33, Appl  |
| 40 | 843.5  | 17.6 | 497  | 2 | US-09-438-185A-20<br>Sequence 20, Appl  |
| 41 | 839    | 17.5 | 866  | 2 | US-09-556-877-189<br>Sequence 189, App  |
| 42 | 839    | 17.5 | 866  | 2 | US-09-620-412C-189<br>Sequence 189, App |
| 43 | 839    | 17.5 | 866  | 2 | US-09-598-419-189<br>Sequence 189, App  |
| 44 | 831.5  | 17.4 | 427  | 2 | US-09-198-452A-31<br>Sequence 31, Appl  |
| 45 | 827    | 17.3 | 483  | 2 | US-09-198-452A-27<br>Sequence 27, Appl  |

## ALIGNMENTS

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RESULT 1
US-09-438-185A-453
; Sequence 453, Application US/09438185A
; Patent No. 6822071
;
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FaalSeq for Windows Version 3.0
; SEQ ID NO 453
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: Cpn0451
US-09-438-185A-453

Query Match      100.0%; Score 4782; DB 2; Length 967;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTSIPWLVSSVLAFLSCHLQSLANBELSPDSEFNGNIDSGTTPKTSATYSLTGDF 60
DB      40 MTSIPWLVSSVLAFLSCHLQSLANBELSPDSEFNGNIDSGTTPKTSATYSLTGDF 99
QY      61 FYEPGKGPLSDSCFQQTNDLTPFGNGSLTFGFIADCTHAGAASTTANKNLTFSGS 120
DB      100 FYEPGKGPLSDSCFQQTNDLTPFGNGSLTFGFIADCTHAGAASTTANKNLTFSGS 159
QY      121 LLSFSSSEPTTYTQGTSLSSAGVNLNIRLVVAGNSTDGGAIKASFLTGTSQD 180
DB      160 LLSFSSSEPTTYTQGTSLSSAGVNLNIRLVVAGNSTDGGAIKASFLTGTSQD 219
QY      181 ALFSNNSSTKGAATATTAGARIANTGVRFSLNSIATSGAIDDEGTSILSNKFLTF 240
DB      220 ALFSNNSSTKGAATATTAGARIANTGVRFSLNSIATSGAIDDEGTSILSNKFLTF 279
QY      241 ENNAKTTGGAICNTKASGSPLLIISNKTLLPASVAETSGAIIHAKLALSSGGTFEE 300
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Db 280 EGNAAKTTGGAICNTKASGSEPELLISNNKTLIFASVAETSOGAIIHAKKALALSSGGFTTF 339
Qy 301 LRNVSSATPKGGAISIDAGSELSLSAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK 360
Db 340 LRNVSSATPKGGAISIDAGSELSLSAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK 399
Qy 361 FTELRAAKNHTIFFYDPTITSEGTSDVLKINNSAGALNPYQGTILFSGETLTADLKV 420
Db 400 FTELRAAKNHTIFFYDPTITSEGTSDVLKINNSAGALNPYQGTILFSGETLTADLKV 459
Qy 421 DNKSSFTQVPSLSGGKLLQKGVLTSESTFSQASGLGMDGTTLTSTAAGTITINIG 480
Db 460 DNKSSFTQVPSLSGGKLLQKGVLTSESTFSQASGLGMDGTTLTSTAAGTITINIG 519
Qy 481 INVDLGLKQPVSLTAKGASNKVIVSGKLNLIIEGNIYESHMFSDQLFSLKITYDAD 540
Db 520 INVDLGLKQPVSLTAKGASNKVIVSGKLNLIIEGNIYESHMFSDQLFSLKITYDAD 579
Qy 541 VDTNVDLSSLLPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFVPSPERKS 600
Db 580 VDTNVDLSSLLPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFVPSPERKS 639
Qy 601 ALVNCNTLMGVFTDRLSLQQLVEIGATGMEHKQGFWVSMNTPLHKTGDENRKGFRHTSG 660
Db 640 ALVNCNTLMGVFTDRLSLQQLVEIGATGMEHKQGFWVSMNTPLHKTGDENRKGFRHTSG 699
Qy 661 YVIGSANTPKKODLFTFAFCHLFARDKDCFIAHNSNRTYGGTLFPKSHTLQPNYLRIG 720
Db 700 YVIGSANTPKKODLFTFAFCHLFARDKDCFIAHNSNRTYGGTLFPKSHTLQPNYLRIG 759
Qy 721 RAKFSESAIEKFPREIPLALDVQVFSHSDNRMEHTHTSLPESGGSWNECIAIGIGLDL 780
Db 760 RAKFSESAIEKFPREIPLALDVQVFSHSDNRMEHTHTSLPESGGSWNECIAIGIGLDL 819
Qy 781 PFVLSNHPHLPKFTIPQMKVEMVYVSONSPRESSDDGSGFISIRLNLSTIPVGAKFVQGD 840
Db 820 PFVLSNHPHLPKFTIPQMKVEMVYVSONSPRESSDDGSGFISIRLNLSTIPVGAKFVQGD 879
Qy 841 IGDSTYTDLSGFFVSDVYRNPPOSTATILVMSPDMSKIRGNI,SRQAFILRGSNYYVNSN 900
Db 880 IGDSTYTDLSGFFVSDVYRNPPOSTATILVMSPDMSKIRGNI,SRQAFILRGSNYYVNSN 939
Qy 901 CELFGHYAMELRGSSRNYNVDVGTKLRF 928
Db 940 CELFGHYAMELRGSSRNYNVDVGTKLRF 967

RESULT 2
US-09-198-452A-478
; Sequence 478, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 478
; LENGTH: 949
; TYPE: PRN
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...949
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-478

Query Match 99.8%; Score 4774; DB 2; Length 949;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 MKTISPMVLVSVLAESCHLQSLANEELLSPPDSFNGNIDSGITPEKTSATYSLTGDF 60
Db 22 MKTISPMVLVSVLAESCHLQSLANEELLSPPDSFNGNIDSGITPEKTSATYSLTGDF 81
Qy 61 FYEPGKGTPLSDSCFQOTDNLFLNGHSLTGFIDAGHAGAASTANKRLTSGS 120
Db 82 FYEPGKGTPLSDSCFQOTDNLFLNGHSLTGFIDAGHAGAASTANKRLTSGS 141
Qy 121 LLSFDSSTPTVTTGGTTLSSAGVNLLENIRKLVNAGNSTADGAIKGAFFLITGSGD 180
Db 142 LLSFDSSTPTVTTGGTTLSSAGVNLLENIRKLVNAGNSTADGAIKGAFFLITGSGD 201
Qy 181 ALFSNNSSSTKGAIAITTAGARIANNVGYRFLSNIASTGGAIIDEGTISLNNKFLYF 240
Db 202 ALFSNNSSSTKGAIAITTAGARIANNVGYRFLSNIASTGGAIIDEGTISLNNKFLYF 261
Qy 241 EGNAAKTTGGAICNTKASGSEPELLISNNKTLIFASVAETSOGAIIHAKKALALSSGGFTTF 300
Db 262 EGNAAKTTGGAICNTKASGSEPELLISNNKTLIFASVAETSOGAIIHAKKALALSSGGFTTF 321
Qy 301 LRNVSSATPKGGAISIDAGSELSLSAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK 360
Db 322 LRNVSSATPKGGAISIDAGSELSLSAETGNITFVRNTLTTTGSTDTPKRNAINIGSNGK 381
Qy 361 FTELRAAKNHTIFFYDPTITSEGTSDVLKINNSAGALNPYQGTILFSGETLTADLKV 420
Db 382 FTELRAAKNHTIFFYDPTITSEGTSDVLKINNSAGALNPYQGTILFSGETLTADLKV 441
Qy 421 DNKSSFTQVPSLSGGKLLQKGVLTSESTFSQASGLGMDGTTLTSTAAGTITINIG 480
Db 442 DNKSSFTQVPSLSGGKLLQKGVLTSESTFSQASGLGMDGTTLTSTAAGTITINIG 501
Qy 481 INVDLGLKQPVSLTAKGASNKVIVSGKLNLIIEGNIYESHMFSDQLFSLKITYDAD 540
Db 502 INVDLGLKQPVSLTAKGASNKVIVSGKLNLIIEGNIYESHMFSDQLFSLKITYDAD 561
Qy 541 VDTNVDLSSLLPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFVPSPERKS 600
Db 562 VDTNVDLSSLLPVPAEDPNSSEYFGQGMNVNMTTDTATNTKEATATWTGTGFVPSPERKS 621
Qy 601 ALVNCNTLMGVFTDRLSLQQLVEIGATGMEHKQGFWVSMNTPLHKTGDENRKGFRHTSG 660
Db 622 ALVNCNTLMGVFTDRLSLQQLVEIGATGMEHKQGFWVSMNTPLHKTGDENRKGFRHTSG 681
Qy 661 YVIGSANTPKKODLFTFAFCHLFARDKDCFIAHNSNRTYGGTLFPKSHTLQPNYLRIG 720
Db 682 YVIGSANTPKKODLFTFAFCHLFARDKDCFIAHNSNRTYGGTLFPKSHTLQPNYLRIG 741
Qy 721 RAKFSESAIEKFPREIPLALDVQVFSHSDNRMEHTHTSLPESGGSWNECIAIGIGLDL 780
Db 742 RAKFSESAIEKFPREIPLALDVQVFSHSDNRMEHTHTSLPESGGSWNECIAIGIGLDL 801
Qy 781 PFVLSNHPHLPKFTIPQMKVEMVYVSONSPRESSDDGSGFISIRLNLSTIPVGAKFVQGD 840
Db 802 PFVLSNHPHLPKFTIPQMKVEMVYVSONSPRESSDDGSGFISIRLNLSTIPVGAKFVQGD 861
Qy 841 IGDSTYTDLSGFFVSDVYRNPPOSTATILVMSPDMSKIRGNI,SRQAFILRGSNYYVNSN 900
Db 862 IGDSTYTDLSGFFVSDVYRNPPOSTATILVMSPDMSKIRGNI,SRQAFILRGSNYYVNSN 921
Qy 901 CELFGHYAMELRGSSRNYNVDVGTKLRF 928
Db 922 CELFGHYAMELRGSSRNYNVDVGTKLRF 949

RESULT 3
US-09-428-122-2
; Sequence 2, Application US/09428122
; Patent No. 6872814
; GENERAL INFORMATION:
; APPLICANT: Comaught Laboratories Limited
; APPLICANT: Mordin et al.
```

; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND  
 ; FILE REFERENCE: 19721-007-019  
 ; CURRENT APPLICATION NUMBER: US/09/428,122  
 ; EARLIER FILING DATE: 1999-10-27  
 ; EARLIER APPLICATION NUMBER: 60/106,046  
 ; EARLIER FILING DATE: 1998-10-28  
 ; EARLIER APPLICATION NUMBER: 60/132,271  
 ; EARLIER FILING DATE: 1999-05-03  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 928  
 ; TYPE: PR1  
 ; ORGANISM: Chlamydia pneumoniae  
 ; US-09-428-122-2

Query Match 38.8%; Score 1855; DB 2; Length 928;

Best Local Similarity 42.7%; Pred. No. 5,7e-131;  
Matches 405; Conservative 171; Mismatches 331; Indels 42; Gaps 20;

QY 1 MKTSTWVUVSSVLAASCHLOSLANEELSPDSDSPNGINDSGTFTKTS---ATTYSLT 56  
 DB 1 MKSSFPKPVSTPAIP--LSMTATETVLDSSASFDGN-KNGNFVRESQEDAGTYLPK 57  
 QY 57 GDVFFYE-PGKGTPLSDSCFKOTTDNLTFLNGHSLTFGFDAGTHAGAA--STANKNL 114  
 DB 58 GAVTLNIPGTGATIKSCFNNTKGDITFTGNGNSLLFCVVDAGTYAAGAAVNSVDKST 117  
 QY 115 TFSGFSLSFSDSPSTVTVTGQGTLS-SAGGVNLENIRKLVAGNFSTADGAIKASFL 173  
 DB 118 TFIGFSLSFISAPSGSITTKGAVSCSTGSLTKNVSLLPKMFSTONGAITAKTSL 177  
 QY 174 LTGTSGDALFSNNSSSTKGAIATAGARIANNVYRFLSNASTSGAIDDEGSIIS 233  
 DB 178 LTGTTSALFSESTSSKGAIGTSDALTITGQGEVSFDNNTSDSGAIFTEASVTLS 237  
 QY 234 NNKFLV----EGNAKT---GGACNTKASGPELISNNKTLIFASVNAETSGA 284  
 DB 238 NNAKVFIDNKVTGASSSTTGDMSGAICAYKTSTDTKVTLTGOMLPSNNITSTAGCA 297  
 QY 285 IHAKULASSGFTFELRNVSAT-PKGAISIDASGELSIAETGNITFVNTLTG 343  
 DB 298 IYVKUELASGGLTFRSNGVGTAPKGAIMIBSGELSLADSGDIYFLNVTYST- 356  
 QY 344 STTPEKRNAINISNGKFTFLRAKNTTFFYPIT--SEGTSSDVLIKINGSAGALNPY 401  
 DB 357 -TPTGTRSSIDLTGTSAMTALRSAGRAIFYDPITGSETTYTVDLVKNETPADSALOY 415  
 QY 402 OGTLFSGETLTADDELKVADNLKSSFTQPVLSGGKLLQGVTLSTSPSOBAGSLIGW 461  
 DB 416 TGNITFTEKLTSEADSKNLTSKLIQPVTLSSGTLSEKGYTLTQATQOADSLEW 475  
 QY 462 DSGTTLSTAGSITITNLTGINVDSLGLKQPVSLTAKASNKVLSGKLNLDIEGNIYES 521  
 DB 476 DVGITTE-PADJSTINNLVINISSIDAKKAKIETATSKNLTLSSGTTLLDPTGFYEN 534  
 QY 522 HNSHDLQSLKITYTADVDVNDVSSLLPVPADPNSTYGOQGN-VNNTTDTATNT 580  
 DB 535 HSLRNPOSYDILBLKASGTVTS---TAVPDPIMGEKFFYGYQGTWGPVWGTGASTT- 589  
 QY 581 KEATATWTKTGFVSPERKALVNTLMGFTDIRLSLOQLVEIGATMEKOGFWVSSMT 640  
 DB 590 --ATFNWTKTGYIPNPERISLVPNSLMAFIDISLHYMETANBELQODRAFWCAGLS 647  
 QY 641 NPLHKTGDNKRGFRATSGGYVIGSANTPKDLPFPAFCHLPARDKCFIAHNSRTYG 700  
 DB 648 NFPHKOSTKTRRGRLHSGGYVIGCNLHTGSDKLSAFCQLGRRDRDYVAAGQGVYV 707  
 QY 701 GTLFPKSHLTQPNVYRLGRAPSESAIEKPREIPLALDOVVSBSHNNKETHYSL 760  
 DB 708 GTLYYQHNET-----YISL-PCKLRPCSLSVVPEIPLVLSGNLSYTHDNDLKTXYTY 761

QY 761 PSEGSWSNECIAGIGLDLPVLSPHPLFTF1PQMKENVVYVSQNSFFESSSDGRGF 820  
 DB 762 PTVKSGWSDSFALEFGARAPICL-DESALFQYMPFKLQVYAHQEGFKGTEARAF 820  
 QY 821 SIGRLNLSIPVGARF-VQDIDGSDTYDLSGFVPSDVYRNPNPOSTATLVMPSPDKING 879  
 DB 821 GSSRLVNLALPIGIRFDEKSDQDA-TYNLTIGYVVDLVRNSPDCITTLRISGDSWKTRG 879  
 QY 880 GNLSROAFLLRGSNNVYVNSNCELFGHYAMELRGSSRYNVVDVGTKLRF 928  
 DB 880 TILARQALVLRAGNHFCEFNSEAFORSFELRGSSRYNVVDLGAKYOF 928

## RESULT 4

US-09-438-185A-449  
Sequence 449, Application US/09438185A

Patent No. 6822071

GENERAL INFORMATION:  
APPLICANT: Stephens, Richard  
APPLICANT: Mitchell, Wayne  
APPLICANT: Kaiman, Sue  
APPLICANT: Davis, Ronald

APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

FILE REFERENCE: 018941-000411US  
CURRENT APPLICATION NUMBER: US/09/438,185A

PRIOR FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: US 60/108,279

PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/128,606

PRIOR FILING DATE: 1999-04-08  
NUMBER OF SEQ ID NOS: 1074

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 449

LENGTH: 937  
TYPE: PR1

ORGANISM: Chlamydia pneumoniae  
FEATURE:  
OTHER INFORMATION: CP0447

US-09-438-185A-449

Query Match 37.5%; Score 1794; DB 2; Length 937;  
Best Local Similarity 42.7%; Pred. No. 2,3e-126;

Matches 404; Conservative 152; Mismatches 353; Indels 38; Gaps 17;

QY 1 MKTSTWVUVSSVLAASCHLO---SLANEELSPDSDSPNGINDSGTFTP-----KTSAT 51  
 DB 10 MKSSLMFLLISSSLALPLSLNFSAPFAVVEINLGFNPSFG--PETYPPAQTINADGT 66  
 QY 52 TYSLTGDFEYFPGKGTPLSDSCFKOTTDNLTFLNGHSLTFGFDAGTHAGAASTAN 111  
 DB 67 INLNDGVSITNAGSTYALTAFCFKETTNLSFGQHGVPFLONIDAGANC-TFTNTAAN 125  
 QY 112 KULTFSGFSLSDSPSTVTVTGQGTLSAGGVNLENIRKLVAGNFSTADGAIKAS 171  
 DB 126 KULTFSGFYSLSL-IQTNATTGTCGAIKSTGACSIQSVSCYFGQNFANDGALQCGSS 183  
 QY 172 FLITGSGDALFSNNSSSTKGAIATAGARIANNVYRFLSNASTSGAIDDEGTSI 231  
 DB 184 ISLS-LNPLVTPAKNKATYKGAIVSTGITTNNLTNSASFENLTANNGALVYBASSF 242  
 QY 232 LSNKFLVEEGN---AAKTTGAI-CNTKASGPELISNNKTLIFASVNAETSGAIIA 287  
 DB 243 ISNKAISFINNSVYATATGTAICSSSTSAKPVUTLSDNDELINIGTALTSGGAIYT 302  
 QY 288 KULASSGFTFELRN--VSSATPVKGAISIDASGELSIAETGNITFVNTLT--TGST 345  
 DB 303 DNVLVSSGGPTLTKNNSAIDTAAPLGAIAIADSGSLISALGSDITTFEGNTVVKASSS 362  
 QY 346 DTPKRNAINIG-SNGKFTFLRAKNTTFFYPITSEGS--SDVLKINGSAGALNPYQ 402  
 DB 363 QTTTNSINIGNNAKIVOLRASQGTIIFYDPITTSITPAULSDALNLNGPDLAQNPAVQ 422

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QY 403 GILFSEETLADLKYADNIDKSFOTOPVLSGGKLLQGVLTLESTFQOEAGSLIGM 462
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DQ 423 GTIVFSSEKISEABAEADNKSSTIOQLTTLIAGQSLSKSGTIVLASFSQSPSTLLMD 482
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 463 SGITLSTTAGSIITNTGAINVDSLGLKQPVSLTKGASNRYVSGKLNLIIDIEGNIYESH 522
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 483 AGTILEFTADG-ITINNVLAVNDISLKETKATLKTKTOASQVFTLISGSLVDPGNGVYEDV 541
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 523 MFESDOLFSLLKITVNDVDVTNNVDISLIPVAPADPRHSEKGFQGMVNMNTTDPATNTE 582
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DQ 542 SWNNPOVFSCTTL--ADDPANHITHDLAADPLEKNPIHWQVQNMALMSOEDITATSKA 599
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 583 ATATWTKTGVPSEPERKSALVCNTLMGVFTDIRSLQOLVEIGATGMHKKGFVWSSMTNF 642
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DQ 600 ATLTWTKTGVPNPERSGTLVANTLMGSEFVDRSIQOLVATKVQSOETGIMWEGISNFE 659
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 643 LHKGDENRKGRFTSGSVYIGSGSAHPKDDLFFACCHLPAPKDCOFIHHNSRTGCT 702
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 660 FHKOSTKINKPFRHISAGTVVGATTLTASDMLTAAFCQLGKORDHPIKKNRASAVAAAS 719
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 703 LFFKGSHTLOPONYLRLGRAKFSESAIEKPREIPLALDVQVSPSHSDNRMETHYTSLPE 762
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 720 LHLQHLATLSPSILRY--LPGSES-----EQVLFDAQISYIGKNTKTYTTOAPK 770
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 763 SEGWSNECTIAGGIGLDLPFVLSNPHPLFKTFIQMKVEMVYVQNSPFESSSD-GRGFS 821
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 771 GESSWYNDGCALELASSLPHATLHSEGLFHAFFPIKYEASYIHQDSFKENNTTLLVRSFD 830
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 822 IGRLLNLSTIPGAKFVQGDIGDSTYYDLSGFVDDVYRNNQOSTATYLVMSPDSSWKIGCN 881
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 831 SGDLINVSVPIGIFPERSRNERBASYEATVIYADVVRKNDPDCITALLINNSTKTTGTN 890
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 882 LSRQAFLLRGSNNYVYNSNCELFQHYAMELALGSSRNRYVDYGTQLRF 928
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 891 LSRQAGIGRAGIFYAFSPNLEVTSLMSLEIGSSRSYVADIGKGFQF 937
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 5
US-09-198-452A-470
; Sequence 470; Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments,
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-470

Query Match: 36.9%; Score 1763; DB 2; Length 930;
Beet Local Similarity 41.7%; Pred. No. 4,9e-124;
Matches 394; Conservative 165; Mismatches 355; Indels 30; Gaps 14;

1 MKTSTIPWLVSSVLAFSCHLOSILAN---EELLSPDSSFENGNSDGTTPPKTSA----TTY 53
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 WKIPHLKLLISTLVTPI-LLSIATYGDASLSPDSDG-AGGSTFPKPSVADANGNTY 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

54 SLTGDVFFYEPEKGTPLSDSCPKQTTDNLTLFGNGHSILTFGTIDAGTAAAGAASTTANKN 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 VLSGVVYINDAGKGTALTGCCFTEETTGDLTFGKGYSFSPFNVVDGSNAGAAASTYADKA 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

114 LTSEGSFLLSPDSSPTVTTGGTLLSAGGVNLEIRKLVAAGVFSTA---DGAIKGA 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 LFTGTSNLSPTAAAGCTTVAASGKSTLLSAGAILNDNGTITLISQVNSMEANNNGAIIYAK 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

171 SFLTLGTSGDALFNNSSSTKGAIAATTAGARIANNGTGVREPLNSIASTSGAIDDEGTS 230

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[illegible]

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RESULT 6
US-09-438-185A-448
; Sequence 448, Application US/09348185A
; Patent No. 6622071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 448

```



```

Qy      643 LKHTGDNKRGKPHRTSGGVIGGSAHPTKDLFFFAFCHLFAAPKDCFIAMNNSRTYGGT 702
      650 FHHDSITXNGFHHISAGYVGGATTTLASDNLITLAFQGLGKRDHFINKRASAYAA5 709
Db      703 LFFKSHHTLQPONYLIRGAKFESAEIAEKFPREIPLADVQVFSFSDNRMETHYLSPE 762
      710 LHLQHLATLSSPFLIRY--LPGSES-----EQVLFDADISYISNTMKTYTQAPK 760
Qy      763 SESMSNCEIAGSIGIDLPFVLSNPHLPKTFEIPQMKEMVYVQNSPFESSSD--GQGFS 821
      761 GESSWINDGCALTLASSLPHTLASHEGLHAYFPPIKVEASTIHODSFKEANTILVASF 820
Db      822 IGRLLNLSIPGAKFVQGDIGDSYTYDLSGPFVSDVYNNQSTATLVKMSDPSNKLIRGN 881
      821 SGDLINVSVDPIGTIFPFRFSRNERASAEYAVIYVADVVRKNDPCTTALLINTSWKTGTN 880
Qy      882 LSRQAFLLRGSNNYVNSNCELPGHAMLELRSSNNYVDVGTGLRF 928
Db      881 LSRQAGIGRAIGFYAPSPNLEIVYNSLMKTRSSSNVYADJGGKQF 927

```

RESULT 8  
US-09-438-185A-447  
; Sequence 447, Application US/09438185A

```

1 GENERAL INFORMATION:
2 APPLICANT: Stephens, Richard
3 APPLICANT: Mitchell, Wayne
4 APPLICANT: Kalman, Sue
5 APPLICANT: Davys, Ronald
6 APPLICANT: The Regents of the University of California
7 TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
8 FILE REFERENCE: 018941-000411US
9 CURRENT APPLICATION NUMBER: US/09/438,185A
10 CURRENT FILING DATE: 2002-03-13
11 PRIOR APPLICATION NUMBER: US 60/108,279
12 PRIOR FILING DATE: 1998-11-12
13 PRIOR APPLICATION NUMBER: US 60/128,606
14 PRIOR FILING DATE: 1999-04-08
15 NUMBER OF SEQ ID NOS: 1074
16 SOFTWARE: FastSeq for Windows Version 3.0
17 SEQ ID NO 447
18 LENGTH: 947
19 TYPE: PRF
20 ORGANISM: Chlamydia pneumoniae
21 FEATURE:
22 OTHER INFORMATION: Cpn0445
23
24 US-09-438-185A-447

```

| Query Match | 36.3% | Score 1734 | DB 2 | Length 947 |
|-------------|-------|------------|------|------------|
|-------------|-------|------------|------|------------|

Best Local Similarity 39.9%; Pred. No. 7.7e-122;  
Matches 378; Conservative 182; Mismatches 356; Indels 32; Gaps 18;

```

QY      1 MTTSTPMVLVSVLATSCHLQSLANBELLSPDSPFNQINDSGF-----TPTKSTATTYL 55
Db      12 MKSSVWMLFFSSSLPLTFSSLSIYAAEVTLSSNNSSYDGS-NGTTFVFSTTDDAAAGTYYSL 70
QY      56 TGDVFEYEEBQG-GTPLSDSCFKQTTDNLTLFLNGSHSLRTGFIADGTHAGAAAATT-ANQN 113
Db      71 LSDVSPQNGALGDIPLASGCFLEAGDGLTFQGNQHLKFAFIWAGSSAGTAVASTADQN 130
QY      114 LTFSGSLSPDSSPSTYTL-TCQGTLLSNAGGVNNENIKRLVAGNPTADGAIKGAASF 172
Db      131 LTFNDSRLSTIISCPLELLSPGQCALKSVGNLSLTGNSQIILPTQNPSSNGGVINATKNF 190
QY      173 LLTGTSGDALFSNNSSST--KCGALATTAGARIANNTRYVRLSNLSTASTSGAIDDEGTS 230
Db      191 LLSGTSGPASFSSNQAFQTKQGVVYATGTTIENSPGIVSPQNLAKSGGALYSTDNC 250
QY      231 ILSNNKFLYPEGN----AAKTGGALCNTKAASSPELLISNNKTLFLASVVALETSGAIIH 286
Db      251 SLTDNQQVFLFDGNSAMEAQAOGGALCTTTDTK--VTLTGNNLSLFTNNALTYGGAIS 308

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OY 287 AKTLAASGCFEPLRANVSSATP---KGAISIDASGEISLASETONIFVRNTLTG 343
Db 309 GLNVSISAGPULP-OSNISGSSAGGGGAINASAGELSLATSDDITF-NNQVYTG 366
OY 344 STDPPKRNAINIGSNGKFTELRAAKNHIIFYDEITBGT--SSDYLKINNGAGALNP 401
Db 367 STST--RNNINIIDPAKTSIRAAQSGIYFYDDPIITPGTAASDTLNLMLADANSEIX 424
OY 402 OGTLISGGETLRADELKAVADNKKSFTPPVLSGGKLLDKQVTLBETSTFSGAGSLCH 461
Db 425 GGAIVSGEKLSPTEKALAAVNTSTIRPPAVLAGDVLRRGVVTPKDLTQSPGSHLM 484
OY 462 DSGTTLSTAGSTITINGINVDSIGLQPVSLAKGASNVIVSGKLNLDIEGNIYES 521
Db 485 DGGTTLISAKEANLSLNGLANVLSLSDGNKAAKLTBAADKNISLSTIALIDIEGSPYEN 544
OY 522 HMFESHDLFSLKTIYDADVDTNVDISLIPVPAEDPNSEYFGOGQNNVATTDITATNK 561
Db 545 HNLKASATPYLLELT-AGANGTITLGLASTLTLQEPETHGYGXGNQLSMA--NATTSK 601
OY 582 EARNTPKTKGVVSPSPRKALCNLTLMKGVTFDIDISLOQVIGATGMENHOGFVWSMTN 641
Db 602 IGSINMTRFGVYPSPERKSNLPLNLSKGNFIDIRINOLITTSKSGFERELMLSGIAN 661
OY 642 FLKTKDENRKGFRHISGCVYIGGSAHTPKDKLFTFACHLFAHDXCFIAHNNSRTYGG 701
Db 662 FFRDMSPIRHRGSRHISGGVALGATATPAEDQLTFACQGFARDRNHITGKNHDTYGA 721
OY 702 TLEPKRSHTL-QPONTYLRGLAKFBESALIEKFRPRTPLALDVQVSPSHSDNRMETHTSL 760
Db 722 SLVFHHEGFDIANFL-WGAKATRAPWVLSISQIIPSTFAKFSYLTIDHMKTYTIDN 780
OY 761 PESGSGWSNECIGAGGLDPFLVLSNPHLPKFTPIPOKAYEMVYVSONSPFESSDGRGF 820
Db 781 SIIGSKRNDAPCADIGASLPFVIVSPY-LKEVNEPFLVKQYIYIAHQODFEREABERAF 839
OY 821 SIGRLNLSIPVGAKEFVQGDIDGDSYTYDLSGFEVSDVYRNNPOSTATLWSPDSWKIRGG 880
Db 840 NKSELINVEIPICVTFERDSKBEKGYDITLTMVYIADVARRNPKCOTSLIASDANMAVGT 899
OY 881 NLSQAPILLAGSNNNYYNSNCELFHYAMELRGLGSRNNVNDVGKRLPE 928
Db 900 NLAQGVSVAAHMFQVNPHEMFLFQGFAEVWSSSRNNTNLGJSFCC 947

```

RESULT 9  
US-09-438-185A-17

```

/ Patent No. 6632671
/
/ GENERAL INFORMATION:
/ APPLICANT: Stephens, Richard
/ APPLICANT: Mitchell, Wayne
/ APPLICANT: Kalman, Sue
/ APPLICANT: Davis, Ronald
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
/ FILE REFERENCE: 0189941-000411US
/ CURRENT APPLICATION NUMBER: US/09/438,185A
/ CURRENT FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: US 60/108,279
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: US 60/128,606
/ PRIOR FILING DATE: 1999-04-08
/ NUMBER OF SEQ ID NOS: 1074
/ SOFTWARE: FastSeq For Windows Version 3.0
/ SEQ ID NO 17
/ LENGTH: 780
/ TYPE: PRS
/ ORGANISM: Chlamydia pneumoniae
/ FEATURE:
/ OTHER INFORMATION: CPn0015
/
US-09-438-185A-17

```

Query Match 33.3%; Score 1593; DB 2; Length 780;  
Best Local Similarity 42.8%; Pred. No. 2,4e-111;  
Matches 338; Conservative 145; Mismatches 275; Indels 32; Gaps 14;

```
QY 153 LVVAGNESTADGGAIKAGASFLLTGTSGDALPSNNSSSTKGAIAATTAGARIANNNGYVRF 212
D 9 LIFSKESTONGAKITAKTSLTGLTWSALFSEVTSKKGAIQTSDALITITGQGEVSF 68
QY 213 LSNIASTSGAIDEGSILSNKFLYF-----EGNAKTT----GGAICNTASSGPEL 263
D 69 SDNTSSDSGAITFEASVTSNNAKVSFIQNKVTGASSSTTGMSGGAICAYKITSIDTKV 128
QY 264 IISNNKTLIFASNVAETSGAIIHAKKLALSSGGFTFELRNVSAT-PRKGAISIDASGE 322
D 129 TLGNQMLFESNNTSTTAGAIYVKUELASGGLTFESRNSVNGCTPARKGALAIENSGE 168
QY 323 LLSIAETGNTTPVARNLTITTTGSTDTPPRNAINIGSNCKTELPAKNTTFYDPTT-S 380
D 189 LLSIADSGDIVLGNVTJST--TPGTRSSSIDLGTSAKMTALRSAGRAIFYDPTTGS 246
QY 381 EGTSSDVLKINNSAGALNPYQGTILFSGETLADDELKADNLKSSFTQVSLSGKLL 440
D 247 STTVTDVLKVNTPPADSALOYTGNIIFTGKLSFTEADSKNLTSKLLQPVTLISGTL 306
QY 441 QKGVLTSTFSQDAGSLGMDSGTLSTTAGSITITNLGINVDSLGLKQPVSLTAKGAS 500
D 307 KKGVTLOTQAFTOQDARLEMDVGTILE-PADSTINNLINISIDAKAKALETKATS 365
QY 501 NKVIVSGKMLIDIEGNIYESHMFSDQLFSLKITVDADVNTVDISLLIPVPAEDPNS 560
D 366 KNLTLSGTITLDPGTGFENHSLRNPOSYDILELKASGTVTS---TAVTPDIMEKEF 421
QY 561 EYGFQGMN-VNMTTDTATNTKATATWTCTGFPSPERSKALVNTLMEVFDI8SLQ 619
D 422 HYEQGTGPIVWGTVGASTT--ATFNWTKGYIPNERIGSLVPNSLMAFIDISLHY 478
QY 620 LVEIGATGMHKKQFVWSSMTNPLHKTGDENRKGFRTSGYVIGSAAHPKDDLFFAF 679
D 479 LMETABEGLQGDRAFWAGLSNPFHKDSTKTRGFRILSGYVIGNLHCTSDKILSAF 538
QY 680 CHLPARDKCFIAHNSRTYGGTLFFGHSHLOPONYLRLGRAKFSSESAIEKPREIPLA 739
D 539 CQFGRDRDYFAKNQGTVYGGTLYQHNET-----YISL-PCRLRCSLSYPTETPVL 592
QY 740 LDVQVSSHNDNMEHTYTSLPSEBSGWSNECIAAGIGLDPFLSLSPHPLFKTFLPQK 799
D 593 FSGNLSTYHTDNDLKTYYTTPYVKGSWGDSPALBFGRAPICT--DESALFQYMPFMK 651
QY 800 VEMVYVQNSFFESSDGRGFSIGRLNLSIPVQAKF-VQDIDGDSYTYDLSGPFVSDY 858
D 652 LQFYVYAHQBGFKEGTAREFGSSRLVNLALPIGIRDKESDCODA-TYVLTIGYTYDLV 710
QY 859 RNNPOSTATLWSPD5WKIRGSLSRQAFLLRGSNNVYNSNCELFGHYAMELRGSSRNY 918
D 711 RSNPDCTTTRISGDSWKTGTNLARQALVLRGNHFCFNSFEAFSGFELRGSSRNY 770
QY 919 NNDVGTGLRF 928
D 771 NVDLGAKYQF 780
```

RESULT 10  
US-09-438-185A-15  
; Sequence 15; Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kalman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 866  
; TYPE: PRN  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: CPN0013  
US-09-438-185A-15

Query Match 30.0%; Score 1435.5; DB 2; Length 866;  
Best Local Similarity 35.9%; Pred. No. 2,1e-99;  
Matches 340; Conservative 147; Mismatches 335; Indels 125; Gaps 15;

```
QY 1 MKTSIHWVSVSYLAFS-CHLOSLAMELLSPDPSFNGNIDSGTFPKTSA-----TTYSL 55
D 26 MKIPLRFLISLVPYLSMGNLGAATTEELASNSFDGTTSTFSKTSATDGTNYVF 85
QY 56 TGDVPFYE-PKGQTPLSDCFKQ--TTDNLTFLGNHSLTFGEFIDAGTAGAA-ASTTAN 111
D 86 KDSVLEENPKGEGTOSTGCFKNDAAAGDNLFGGGSFSTFSNIDATTASGAISGEANV 145
QY 112 KNLTFSGFSLSPDSSPTVTTGQTLSSAGCVNLEIRKLVVAGNFTADGAIKAGS 171
D 146 KYVTLISGFSALGFLKSPASTVTTGALINVKGLSLDDNDKVLIDQNFSTGOGAINCAG 205
QY 172 FLITGTSGALPSNNSSSTKGAIAATTAGARIANNNGYVRFSLNISTSGAIDDEGT91 231
D 206 ----- 205
QY 232 LSNKFLYEGNAKATTGGAICNTKASGSPBELIISNNKTLIFASNVAETSGAIIHAKKLA 291
D 206 -----SLKIANKSLSFIGNSSSTRGAIHTRKNTL 235
QY 292 LSSGFTFELRNVSATPRKGAISIDASGELSLSAETGNTFFVNTLTGTSSTDPKRN 351
D 236 LSSGGETLFGQNTAPPAAGKGAIALADSGTSLISGDSGDIIFEGNTI---GATGVSHS 292
QY 352 AINIGSNKFTELRAKNTTFFYDPTISEGSS--DVLKINNSGALNPYQGTILFSG 469
D 293 AIDLGSAKITLRAAQGHITFYDPTITVGTSTVADALNINSPDTGDNKEYTGTIVFSG 352
QY 410 ETLTADELKVAADNLKSSFTQPVSLSGKLLQKGVLTLESTSFQDAGSLGMDSGTTLST 469
D 353 EKLTEBADEKKNRTSKLLQNVAFKNGYVLKQDVLSANGFSQDANSKLIIMDLGSLVA 412
QY 470 TAGSITITNLGINVDSLGLKQPVSLTAKGASNKVIVSGKMLIDIEGNIYESHMFSDQL 529
D 413 NTESEITLVEINIDSLRNGKKIKLSAATAQKDIRDRPVLAISDESFYQNGFLNEDHS 472
QY 530 F-SLAKITVDADVNTVDISLLIPVPAEDPNSGTGQGMNVNMTTDTATNTBEATATWT 588
D 473 YDGLLELDAGKDIVISADRSIDAV-----QSPYGYQGKMTJINWSTD---DKKATVSWA 523
QY 589 KTGVPSPERKSLVNCNTLMGVFTDTRSLQQLVEIATGMEHKGFWSSMTNPLHKTGD 648
D 524 KQSFNPTAQEALVNLMLGSLIDRSQNFTELCTBEGAPYKRRVWAGISVLRSGR 563
QY 649 ENRKGFRHTSGGVVIGSAAHTPPKDLFTPAFCHLPARDYDCTFIHNSRTYGGTLFPKIS 708
D 584 ENQRKFRHVSGGVVAGSTRMPGDDTLISGFQOLFARDXDYFNMNTFAPTYAGSLRLQHD 643
QY 709 HTLQPVNYLRLGRAKSESAIEKPREIPLADVQVSPSHSDNRKMTHTSLP----- 761
D 644 ASLVSYSVTLBGGGLRETLPLPVYSKTLPCSFYQGLSYGHTDHRMKTB--SLPPPTLS 701
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[illegible]

RESULT 11  
US-09-438-185A-6  
; Sequence 6, Application US/09438185A

```

; PATENT NO: 6622071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 932
; TYPE: prt
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: Cpn0005
; US-09-438-185A-6

```

|                       |                   |                    |            |             |
|-----------------------|-------------------|--------------------|------------|-------------|
| Query Match           | 28.3%;            | Score 1355;        | DB 2;      | Length 932; |
| Best Local Similarity | 35.4%;            | Pred. No. 2.7e-93; |            |             |
| Matches 339;          | Conservative 155; | Mismatches 399;    | Indels 64; | Gaps 21;    |

```

QY      3 TSIPWLVSSVLAEFCHLOSLANEEL-----LSPPDSFNGNIDSGTFTTPKTSA--TTSLSL 55
Db      9 TKMRFSLCGFPLVFEFTLLSVFDTLSAFTTSLTFPDSFHHGSOAERSYNYOQADVYSL 68
QY      56 TGDVFYFEBGKCTPLSDSCFQKTTNNLFLGNGHSLTGEFIDAGTHAGAAASTANKUL 115
Db      69 TGDVSIISNV--DNSALNKACFNVTSSGVTLPAGHHGLYFNINISSGTTKGCALCCODPOAT 127
QY      116 --FSGFSLSPDSSPSTTVTTQGTLSAGVNLNIRKLVVAGNFSTADGAIKGAFTL 173
Db      128 ARFSGPSTLFIQSPGD--IKQGCGLSKMLMLNNYVVRPEQNSKTKGALISGANVT 185
QY      174 LTGTSGDALFSNNSSSTKGAIAATAGARIANNTRYRLSLIAST--GGALIDDEGTSIL 232
Db      186 IVGNVDSVSEFYON--AATFGAIIHSSGPLOIAVNOAIEIPAQNTAKNGSGGALYSGDIDI 244
QY      233 SNKKFLYPEGNAAKTT---GGAINCTRKASG---PELIISNNKTLIPASVVAETSGGA 284
Db      245 DONAYVLPRENALTLTAIGKGAIVCCLPFGSSSTPVIYFSDNKQLYVERHHSIMGGA 304
QY      285 IHAKKALISSGGFTFELRNNVSSATPK--GGAISIDASGELSIAETGNITFVRNLTLT 342
Db      305 IYARKLSTISSGGPTLFI--NNISYANSQNGAIAIDTGEIISLAEKGTITFOGN----- 358
QY      343 GSTDPPKRNAINIGSNGKFTLELRAKNHTIIFYDDPTTSGTSDVUKIINNSAGALNPQ 402
Db      359 -RTSLPELNGIHLLQNAKFLKIQARNGSIIEFYDPTTSADGSTQTLNINDGPRN--KEYT 415

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0Y      GTILFSGGTLVADEKLVADNKNKSSEFTQVVSJSGGKILLLOKQVTLLESTSPSGAGSLLGMD 462
403      GTILFSGGTLVADEKLVADNKNKSSEFTQVVSJSGGKILLLOKQVTLLESTSPSGAGSLLGMD 462
416      GTILFSGGKSLANDR---DFKSTTIPQVNVLSAGTLVIREKGAENVVSKRTQSGPBGHLYVD 472
0Y      463      SGTTLSTTAGSITTTNGLINVDLSGLKQPVSLTAKGASNKVIVGKLNLDIEGNIYES 521
473      LGTKILAKEDIALITGLAIDIDISLSSSSSTAAYIKANTANKOISTVDSIELISPTGAAYTD 532
0Y      522      HMFHSDOJFSLTKITVDADVDTNVDISLIPVADPNSEYFQOGOMVNMVMTDTATNTK 581
Db      533      LMRMSQTFPRLSLLEPGAGSGVTYVAGDFLPV-----SPHYFQGNWKILAM---TGTGNK 584
0Y      582      EATATWTKTGFEVPSPERKSALVCNTLWGVFTDILSLQOLVEIGATGMENHKOGFWWSMTN 641
Db      585      VGEEFMDKINIKYFPRBEKGNLVPLNIMGAADVRSILMOQOEHTASSLQTDRLIMIDIGION 644
0Y      642      FLHKTGDNRRKGFRHTSGGVYIG-GSATHPKXDLPTPAFCHLPADKOCFELHNNRSRTG 700
Db      645      FFHVSASEDNIRYRINSGGYLVSUNNETPK-HYTSMAFSQLPKSDKQYAVASNNETRMVL 703
0Y      701      GTLFPRKSHTL-----OPONYLRIGRAKESSEALIEKPREIPLALDVQVSPESHSDN 751
Db      704      GSLYLYQYTTSLGNIIPRYASRBNPNVNVGILSRFFLQNP-----MIRFLCAYAHANT 755
0Y      752      RMEHTIYTLPEBEGSMNECTAGAGIGDLRFVLSNPHYFKTFIPOMKEMVYVUSNSFF 811
Db      756      DMKTDYANFPMVKNSWRNNCWALIECGGSGPRLVLFENGRLFFQCALIPMKIQLYVAYGDPK 815
0Y      812      ESSSDGSGFSIGRLNLISLIPVAKKVVQGDIGDSTYDLSGFEVSDVYRNNPOSTATLVMS 871
Db      816      ETTAAGRFRFNSGSLNISVPLGIRREKALASQDVLVDFSFYIPIDFRQDSCBALVVIS 875
0Y      872      PDSWKIRGNSLRQAFLLRGSNNYYNSNCELFGHYAMELRSSSRRYNVNDVGTKLRF 928
Db      876      GDSWLVPAHAYSRNAFVSGTGRYHFNNDVTELLCGSIECRHARYANINCSKEFF 932

```

RESULT 12  
US-09-198-452A-15  
; Sequence 15, Application US/09198452A

```

/ GENERAL INFORMATION:
/ APPLICANT: Griffiths, R.
/ TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
/ TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
/ TITLE OF INVENTION: and treatment of infection
/ FILE REFERENCE: 9710-003-999
/ CURRENT APPLICATION NUMBER: US/09/198,452A
/ CURRENT FILING DATE: 1998-11-24
/ NUMBER OF SEQ ID NOS: 6849
/ SEQ ID NO 15
/ LENGTH: 922
/ TYPE: prt
/ ORGANISM: Chlamydia pneumoniae
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: 1...922
/ OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-15

```

|                       |                   |                    |            |             |
|-----------------------|-------------------|--------------------|------------|-------------|
| Query Match           | 28.1%;            | Score 1345;        | DB 2;      | Length 922; |
| Best Local Similarity | 35.4%;            | Pred. NO. 1.5e-92; |            |             |
| Matches 335;          | Conservative 154; | Mismatches 393;    | Indels 64; | Gaps 21;    |

```

QY 14 LAFSCHLOSLAAEEL-----LSPDSFNGNIDSGHFRTKTA-TTYSLGVDFYFEPGK 66
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 10 LVFSFTLSVPTSLSATITSLTPBSFPGDQGNARSLNVQAGDVYSLTGDVLSINV-D 68
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 67 GRPLSDSCKQKOTINDLIFLGNGHSLTFGIDAGTHAGAAASTAMKNTL--EEGFSLTF 124
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 69 NSALNACPKVTVSGSVTFPAGNHGXVFNNISSTITTEGAVLCQDDQATRRFGFSTLS 128
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 125 DSSFTVTYTGQGLTSSAGVNLNIRKLVAAGNFTADGALKGASFLITGTSGDALFS 184
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```



|   |   |     |  |     |
|---|---|-----|--|-----|
| D | b | 129 | NOSPED--IKEGCLYSKATMLLNNVYVREFEONSKTGGALSGANVTIVGNIBDSVSTY     | 186 |
| Q | y | 185 | NNSSSTKGCAIATTAGARIANNTRYVFLSNIAST--SGGALIDEGTSILNNKFYLEGN     | 243 |
| D | b | 187 | ON-AATFGGAIHSSGPLQIANVQAEIRFAONTAKONGSGALVSDGDIDIDQNAVYLFREN   | 245 |
| Q | y | 244 | AAKTT----GGAICNTKASGS----PELLISNNKTLIPASNAVETSGGAIHAKKALSSG    | 295 |
| D | b | 246 | EALTTAIGKGGAVCCLPTSGSTPVPVITPFSNNKOLYFERHNSIMGGAIYARKLISISSG   | 305 |
| Q | y | 296 | GTFEFLRNNVSATPK--GGAISIDASGELSIAETNGNTTFPRNTLTGTSDDTPKRNMI     | 353 |
| D | b | 306 | GPTLFTI--NNISYANSQNLGALAIADTGGELISLSAEKGIITFGQN-----RTSLPLNGI  | 358 |
| Q | y | 354 | NIGSNGKFELELRAAKNHTIFPYDPIITSESTSSDVLKINNGSAGALNPYOGTILFSGETLT | 413 |
| D | b | 359 | HLQNAKFLKIQARNGYSIEFYDPIITSEADSGTQUNINDPNK--KEYITGILIFSGEKSJ   | 416 |
| Q | y | 414 | ADELKVADNLKSSFTQPVVSLSGCKLILQKGVTLLESTFSGQEAQSLIGMDSGTLSTTASG  | 473 |
| D | b | 417 | ANDPR---DFKSTIPQNNVLISAGYLVIKKEGAEVTSKFTQSPGSHLVLLDGLTKLASKED  | 473 |
| Q | y | 474 | ITITMLGINVDSLGKQPVSLTAKGASNVI--VSGKLNLDIBGNLYESHMNSHDLFEL      | 532 |
| D | b | 474 | IAITGLAIDIDBLSSTRAIVKANTANKQISVTSIELISPTGNAYEDLRMNSOTFPL       | 533 |
| Q | y | 533 | LKITVDADVDTNVADISSILPVAEPDENSEYFGQOGQNVMTDTDTATKEATATWTKTGF    | 592 |
| D | b | 534 | LSLEBAGAGSYYVYAGDPLV-----SPHYQOGNKKLAM---TGKNKVGEPFWKIXY       | 585 |
| Q | y | 593 | VSPERKSAVCNTLMGVFTTDIRSLQOLVEIGATGMEHKQGFVWSMFTLHKTDENRK       | 652 |
| D | b | 586 | KPREPEKGNLVENILMGNAVDRSLMQVETHASSIQOTRGIMIDIGMLPHVSASEDMI      | 645 |
| Q | y | 653 | GFRHTSGGVIG--GSAHTPKDLPFPAFCHLTARDQDCIANNNSTTYGTLFPFKISHLT     | 711 |
| D | b | 646 | RYRHNSSGVYIVSNNEITPK--HYTSMASFQLSRSDVAVSNNEYMYLGSYLQYTTBL      | 704 |
| Q | y | 712 | -----OPONYRLGRAPKFSESAIEKFPREIPLADVOVSFSHSDRMETHYSLBE          | 762 |
| D | b | 705 | GNIRPYARBNPNNVNGILSRRLQNP-----MIHFPLCAYGIAHTDMKTDIVANFPM       | 756 |
| Q | y | 763 | SEGSWSNECIAGIGLDLPFLVLSNPHLPKTEIPOMKVEMYVVSQNSPRESSDGRGFSI     | 822 |
| D | b | 757 | VKNSRBNNCWALIECGSMPLVLFENGRLFLQGAIPFMKQLVYAYQGDFFETTLADGRFEN   | 816 |
| Q | y | 823 | GRLLNLSPVGAKFVQGDIGDSYTTDLSCGFVYSDVYRNNPOSTATLWMSPDSKTIKGNL    | 882 |
| D | b | 817 | GLSTISIVPLGIRFEKALISQDVLVDFSFYSYIPDIFRKPSCCEALIVIGSDSWLPAAHV   | 876 |
| Q | y | 883 | SROAFLLGNSNNVYVNSNCELFCHAMELRRGSSRRNNVUVGKLRP                  | 928 |
| D | b | 877 | SRHAFVSGTGRYHNDYTELLCRGSIICERPHARRNNINCGSKFRP                  | 922 |

RESULT 13  
US-09-438-185A-451  
Sequence 451, Application US/09438185A  
Patent No. 6622071  
GENERAL INFORMATION:  
APPLICANT: Stephens, Richard  
APPLICANT: Mitchell, Wayne  
APPLICANT: Kaiman, Sue  
APPLICANT: David, Ronald  
TITLE OF INVENTION: The Regents of the University of California  
FILE REFERENCE: 018941-000411US  
CURRENT APPLICATION NUMBER: US/09/438, 185A  
CURRENT FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: US 60/108, 279  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/128, 606

```

; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 451
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0449
; US-09-458-185A-451

```

|                       |                  |                   |           |            |
|-----------------------|------------------|-------------------|-----------|------------|
| Query Match           | 26.9%            | Score 1286        | DB 2      | Length 634 |
| Best Local Similarity | 41.5%            | Pred. No. 2.4e-89 |           |            |
| Matches 268           | Conservative 117 | Mismatches 225    | Indels 32 | Gaps 10    |

|    |     |   |     |
|----|-----|---|-----|
| Qy | 295 | GGFPEFIRANVSSATP-KGGAISIDASGEISLAEQNTIFVRNTLTGGSTDTPKRAAI     | 353 |
| Db | 9   | GGGISFNNNTVOGTTAANGGAISISILAAGEGSLSAEADITFNCAIAVAT-TPQYTKRASI | 67  |
| Qy | 354 | NIGSNGKFTELRAKKNHTIFFEYDITGE--GTSADVAKINNGSAGALNPYGGTILFSGET  | 411 |
| Db | 68  | DISGTAKITMLRAISGHSIFFYDITANTADSTDTLNLKAKDAGNSTDVSGSIVFSEK     | 127 |
| Qy | 412 | LTADELKVNADLKSSFTQPVSLSGKLLLOKGVTLBSTSPSOEAGSLGDSGTTLLSTA     | 471 |
| Db | 128 | LSBEDAKAADNLSTLQKPYTLTLAGNVLTKRGVTLDTKGFTQSGSSVIMDAGTTLKAST   | 187 |
| Qy | 472 | GSITITMLGINVYSLGKOPVSLAKGASKVIVSGKLTNLDIEAGNIYESHMFHDOLFS     | 531 |
| Db | 188 | BEVTLTJLSTIPVBSLGEKKVVIASAASKNVALSGPILLDNDGNNAYENHDLOKTDQFS   | 247 |
| Qy | 532 | LKLTIVADVDVTVNDISLSLIPVPAEDPNSEYGFQGNVNVMTTDTAT--NTKEATATWTK  | 589 |
| Db | 248 | FVQJSA-LGTATTTDVA---VPTVAPRTHGXGYGTGWTMTVDDTASNPKTKATLAWTN    | 303 |
| Qy | 590 | TGVPSPERKSALVYCNLTMLGVTFVDIRBSLOQLVEIGATGMHEKQGFVWSMTNPLHKTGE | 649 |
| Db | 304 | TGYIPNERGQPLVPSNLWGSFSDIOAIQGVTERSAITLCSDRGFMAAGVANFLDKCKG    | 363 |
| Qy | 650 | NRKFRHTSGGYVIGGSANTPKODLFFAFCHLFARDKDCFIAANNSRYGTLFFKXSH      | 709 |
| Db | 364 | EKKRYRHKSSGYAIGAAQTCSEKLSIFACQJFGSKDFLVANHMTDTYAGARYIHIT      | 423 |
| Qy | 710 | TLOPQNYLRLGRAKFESSAIEKFP--REIPLALDVYVSSHSDNRMEHTYLSLPESEGS    | 766 |
| Db | 424 | EC-----SFFIGLCCLDKLPGSWSHKLPLYEGOLAAVSHVNSDKTKXTTAPREVYGS     | 473 |
| Qy | 767 | WSNECINGIGLDBPFLSNPMP---LFTFTPQMEVEMVYQNSFPFESSQGRGSI         | 822 |
| Db | 474 | WGNNAFNMMLGAS-----SHSYEPYLHCFTTYAPYIKLNLITYIKQDSFSEKGTGRSTD   | 528 |
| Qy | 823 | GRLNLISIPVGAKFVQGDIGDYYTYDLSGEFVSDVYRNNPOSTATLVMSPDWKIRGNTL   | 882 |
| Db | 529 | SNLPNLISLPITGVKFEKPSDCNDFSYDITLTVPLDIRNDEPKTALYISGASMETYANL   | 588 |
| Qy | 883 | SRQAFLLRGSNNVYMNCELFHYAMELIGSSSNVYVNDCTKARF                   | 928 |
| Db | 589 | ARQALQVRASGHYAFSPMEFVLTQFVEYEVGSSSTIVNDVIGKQF                 | 634 |

```

RESULT 14
US-09-198-452A-474
; Sequence 474, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevent
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849

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! SEQ ID NO 474  
! LENGTH: 643  
! TYPE: PRT  
! ORGANISM: Chlamydia pneumoniae  
US-09-198-452a-474

Query Match 26.9%; Score 1286; DB 2; Length 643;  
Best Local Similarity 41.5%; Pred. No. 2.5e-88;  
Matches 268; Conservative 117; Mismatches 229; Indels 32; Gaps 10;

Qy 295 GGFPEFLRNVSATKP-KGGAISIDASGELSLSAETGNIPTVTRTLTTGSDTPKRNAI 353  
Db 18 GGGISFNNTIVQGTGAAGAISSILAAGECSLSAEDDITFNGAIVAT-TPQTTKXNSI 76  
Qy 354 NISNGKFTELRAKNHTIFFYDPTSR--GTSADVLIKINNGSAGALNPYOGTTLFSGET 411  
Db 77 DIGTAKITNLRAISGHSIFPYDPTANTADSTDTLNLKADAGNSTDVSGLVPSGEK 136  
Qy 412 LTADELKVDNLKSSFTQVPSLSGGKLLQKVTLESTFSQEAAGSLGMDSGTTLSTTA 471  
Db 137 LSEDEAKVADNLSTLQKQVTLTLAGNLVLRKGVTLDTKGTGQTGASSVIMDAGTTLKAST 196  
Qy 472 GSITTTMLGNVDSGLKQPVSLTRAKASNKVIYSKLNLDIGNIYESHMFSDQLFS 531  
Db 197 EEVTLTGSLIPVDSLIGBKRVIAASAKXVALSGPILLDNGQAMENHDLCKTQDFS 256  
Qy 532 LKKTIVADVDTNDISLIPVPAEDPSEYGFQGGOMNVNMTDTAT--NTKEATATWTK 589  
Db 257 FVQJSA-LGTTTITTDVPA---VPVATPTTHKGYGTGCMTAVDDTASPTKTKTTLAMTN 312  
Qy 590 TGFVPSPERKALVNTLMGVFTDIRSLQQLVEIGATGMEHKGFVWSMTNPLHKTGDE 649  
Db 313 TGYLPNPERQPLVNSLMSGFSFDIQAIOGVIERSSALTLCSDRGFMAGVANFLDKDKG 372  
Qy 650 NRKQFRHTSGGVVIGSGAHTPKDLPFAFCHLFAKDQCIIANNRTYTGTLFFGSH 709  
Db 373 EKRRYRHSGGVYALGGAQTCSENLISPAFCQSGSDPLVANKHDTYAGAAVYIHT 432  
Qy 710 TLQONVYLRGRKPFSESAIEKFP---REIPLADVOVSFSHSDNRMETHTYSLPESGS 766  
Db 433 EC-----SGFIGLCLKLPGSMHKLVEGQLAHSVNDLTKTKTAPEYKGS 482  
Qy 767 WSNECIAGIGLDLPVLSNPHP---LKFPTIPQMKVEMYVVSQNSFESSSDGRFSI 822  
Db 483 WGNNAFMNLGAS-----SHSYPEYLHCFDTYAPYIKLNTLYIKQDSFEKGTGRSPDD 537  
Qy 823 GRNLNLSTPVAKPQVQSIGDSTYDLSGFVSVSVYRNKPOSTATLVMSPPSMKIRGNL 882  
Db 538 SNLFVLSLPVIGKKEKFDSCNDPFDLTLSVYPLDIRNDPCTTALVLISGASWETYANNL 597  
Qy 883 SROAFLLRGSNNVYVNSNCELFGHYAMELRGSSSRNRYNDVGTKLRF 928  
Db 598 ARQALQVAGSHYAFSPMFVULGQVFPEVRGSSRLYNDVLGKQCF 643

RESULT 15  
US-09-438-185A-455  
Sequence 455: Application US/09438185A

Patent No. 6822071  
GENERAL INFORMATION:  
APPLICANT: Stephens, Richard  
APPLICANT: Mitchell, Wayne  
APPLICANT: Kaiman, Sue  
APPLICANT: Davis, Ronald  
TITLE OF INVENTION: The Regenes of the University of California  
FILE REFERENCE: 018941-000411US  
CURRENT APPLICATION NUMBER: US/09/438,185A  
CURRENT FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: US 60/108,279  
PRIOR FILING DATE: 1998-11-12  
PRIOR APPLICATION NUMBER: US 60/128,606  
PRIOR FILING DATE: 1999-04-08

! NUMBER OF SEQ ID NOS: 1074  
! SOFTWARE: FastSeq for Windows Version 3.0  
! SEQ ID NO 455  
! LENGTH: 999  
! TYPE: PRT  
! ORGANISM: Chlamydia pneumoniae  
! FEATURE:  
! OTHER INFORMATION: CPN0453  
US-09-438-185A-455

Query Match 26.9%; Score 1284.5; DB 2; Length 999;  
Best Local Similarity 32.8%; Pred. No. 6.1e-88;  
Matches 332; Conservative 163; Mismatches 393; Indels 125; Gaps 27;

Qy 1 MKTSIWWVSVIATFSCHLOSILANEELSPDPSFNGNIDSGTTPKTS----ATTYSL 55  
Db 27 MKSIRKFLISTLA-PCFASTAFVEIVMPSNFDGS--SGKIFPYTLSDPRGLCIF 83  
Qy 56 TGDVFFPEPKG-TPLSDSCFKQTTNLTFLNGHSLTFGFDAGTHA-GAAASTTANON 113  
Db 84 SGLDIYANLDMNISRTSSCFNRAGALQILKKG--VPSFLNIRSSADGAALISVITON 141  
Qy 114 -----LTFGFSLSLSDSSPTVT----- 134  
Db 142 PELCPUSFSGFSOMIFDNCESLTSDSASNVIPHASAIYATPMLFTNNDSILFOYNRSA 201  
Qy 135 GCGTLLSAGVNLNENIRK-LVVAGNFSTADGAIKG-AGFLTGTSGDALFSNNSSITKG 192  
Db 202 GFQAAIRGHSITILENTKSLFPNGSISNGALTSAAINLINSAPVIFSTNAGIYG 261  
Qy 193 GAIAITTAGARI-ANNNGYRFLSNINASTSGAIDDEGTSLSNNKFLYPEGNAAKTT--- 248  
Db 262 GAIVLTGSMVLTGNSLVGFVNN-SSRSGAIVANGNVTFNSNDLTFQNTASPNLSL 320  
Qy 249 -----GGAI-CNTKASGP---ELIISNNKTLIFASVVAETSGAIIH 286  
Db 321 PAPTPEPTPAVTPLLIGYGALICTPPATPPPGVSLITSGENSVTFLINIASBOGALLY 380  
Qy 287 AKKLALSSGFTPEFLNNVSSATPKGAISSIDASGELSLSAETGNITFVANTLTTGSTD 346  
Db 381 GKISIDSNKSTIFLNGTAG---KGAIALIPSGELSLSANGDILLFNKNLSITSG--- 433  
Qy 347 TPKRNAINISNGKFTELRAKNHTIFFYDPTSE---GTSADVLIKINNGSAGALNPYOG 403  
Db 434 TPTRNSIHFKDKAKFATLGAQGYTLTYFYDPIRSDLSAASAAATVAVPKASADAYGG 493  
Qy 404 TILFSGEFLTADKXADNLKSSFTQVPSLSGGKLLQKVTLESTFSQEAAGSLGMDS 463  
Db 494 TIVFSGEFLTATEBAPANATSTLNLQKLEGGTLALRNGATLVNHNFTODEKSVYIMDA 553  
Qy 464 GTTLST-----TAGSITITNLGINVDSGLKQVSLTRAKASNKVIYSGKMLLDIEN 517  
Db 554 GTTLATNGANNNDGATTLNKLVINLDSLDGTAAVNVNGSTGALLTISGLIVKNSQD 613  
Qy 518 IYESH-MFSDH-QFLSLKITTVDADVDTNDISLIPVPAEDPNSERGFQGGOMNVNMTTD 575  
Db 614 CODHGMFNKDLQVPLIELKATSNVTYTTDFSLGTVGQOSP---YGYGTV--EFTID 668  
Qy 576 TATNTKATATMTKGTQVPSPERKALVNTLMGVFTDIRSLQQLVEIGATGMEHKGFV 635  
Db 669 TTHIT--VTGNWKKTGVLPHPERLAPLIPNSLVANNYIDLAAVQASAADEVDYGRKO-LS 725  
Qy 636 VSSWTFELAKTGDENRKGRPHRTSGGVYIGSAHTPKDLPFAFCHLFAKDQCFIAHNN 695  
Db 726 ITGTLNFFHANHGDAASYRHMGGVILNITYTITTPAALSIGFGQFTSKXYLVHGH 785  
Qy 696 SRTYGGTLFFKHSHTLOPQNYLGRKPFSESAIEKFPREIPLALDVQVSFSSDNMET 755  
Db 786 SNVFAIVYGNITKSL-----FGSSRFSGGTSR-----VYSSNSNEKYKT 826  
Qy 756 HTYSLPESGSWSNECIAGIGLDLPVLSNPHLPFTFIPQMKVEMYVVSQNSFESS 815  
Db 827 SYTKLPGRCSWSNMCWLGELBNLPTLSSRLNLKQIIPVAKAEVAVATHGIGIENTP 886



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## OM protein - protein search, using sw model

Run on: November 25, 2005, 14:03:16 ; Search time 2.56424 Seconds  
(without alignments)  
1096.908 Million cell updates/sec

Title: US-09-446-677B-2

Sequence: 1 MKTSLPWLVSIVLAFSCHL.....MEIRGSSRMVNVDTKLRP 928

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

## Database :

Published Applications AA New:  
1: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep: \*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep: \*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep: \*  
4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep: \*  
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6: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep: \*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep: \*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep: \*

\*Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                 | Description          |
|------------|-------|-------------|--------|--------------------|----------------------|
| 1          | 187.5 | 3.9         | 1992   | US-11-013-759-3    | Sequence 3, Appl1    |
| 2          | 187.5 | 3.9         | 1992   | US-11-013-759-13   | Sequence 13, Appl1   |
| 3          | 187.5 | 3.9         | 2047   | US-11-013-759-4    | Sequence 4, Appl1    |
| 4          | 187.5 | 3.9         | 2047   | US-11-013-759-7    | Sequence 7, Appl1    |
| 5          | 172   | 3.6         | 2053   | US-11-013-759-9    | Sequence 9, Appl1    |
| 6          | 171   | 3.6         | 761    | US-10-485-517-252  | Sequence 252, Appl1  |
| 7          | 169.5 | 3.5         | 2314   | US-11-013-759-11   | Sequence 11, Appl1   |
| 8          | 141.5 | 3.0         | 496    | US-10-485-517-324  | Sequence 324, Appl1  |
| 9          | 141.5 | 3.0         | 496    | US-10-485-517-325  | Sequence 325, Appl1  |
| 10         | 140.5 | 2.9         | 1155   | US-10-793-626-1780 | Sequence 1780, Appl1 |
| 11         | 137.5 | 2.9         | 802    | US-10-510-386-2    | Sequence 2, Appl1    |
| 12         | 124.5 | 2.6         | 1332   | US-11-091-643-18   | Sequence 18, Appl1   |
| 13         | 122   | 2.6         | 1196   | US-10-667-295-100  | Sequence 100, Appl1  |
| 14         | 119.5 | 2.5         | 457    | US-11-074-176-12   | Sequence 12, Appl1   |
| 15         | 119.5 | 2.5         | 1126   | US-10-485-517-248  | Sequence 248, Appl1  |
| 16         | 118.5 | 2.5         | 444    | US-11-074-176-170  | Sequence 170, Appl1  |
| 17         | 118.5 | 2.5         | 1076   | US-10-131-826A-219 | Sequence 219, Appl1  |
| 18         | 117   | 2.4         | 318    | US-10-802-796-727  | Sequence 727, Appl1  |
| 19         | 117   | 2.4         | 392    | US-10-793-626-2494 | Sequence 2494, Appl1 |
| 20         | 116   | 2.4         | 2721   | US-11-096-051-10   | Sequence 10, Appl1   |
| 21         | 116   | 2.4         | 2725   | US-11-096-051-8    | Sequence 8, Appl1    |
| 22         | 115   | 2.4         | 1386   | US-11-091-643-6    | Sequence 6, Appl1    |
| 23         | 114   | 2.4         | 1290   | US-10-485-517-141  | Sequence 141, Appl1  |
| 24         | 112.5 | 2.4         | 758    | US-10-485-517-144  | Sequence 144, Appl1  |
| 25         | 111   | 2.3         | 1572   | US-10-793-626-2906 | Sequence 2906, Appl1 |

|    |       |     |      |   |                    |                      |
|----|-------|-----|------|---|--------------------|----------------------|
| 26 | 110   | 2.3 | 692  | 7 | US-11-045-802-26   | Sequence 26, Appl1   |
| 27 | 110   | 2.3 | 1332 | 1 | US-10-821-234-914  | Sequence 914, Appl1  |
| 28 | 110   | 2.3 | 2376 | 7 | US-11-096-051-4    | Sequence 4, Appl1    |
| 29 | 110   | 2.3 | 2715 | 7 | US-11-096-051-2    | Sequence 2, Appl1    |
| 30 | 109   | 2.3 | 1047 | 1 | US-10-510-386-200  | Sequence 200, Appl1  |
| 31 | 108   | 2.3 | 1432 | 1 | US-10-510-386-218  | Sequence 218, Appl1  |
| 32 | 107   | 2.2 | 1119 | 7 | US-10-131-826A-352 | Sequence 352, Appl1  |
| 33 | 106.5 | 2.2 | 934  | 7 | US-11-108-864-19   | Sequence 19, Appl1   |
| 34 | 106   | 2.2 | 334  | 1 | US-10-802-796-728  | Sequence 728, Appl1  |
| 35 | 106   | 2.2 | 567  | 1 | US-10-485-517-216  | Sequence 216, Appl1  |
| 36 | 106   | 2.2 | 877  | 1 | US-10-485-517-200  | Sequence 200, Appl1  |
| 37 | 103.5 | 2.2 | 4384 | 1 | US-10-821-234-1120 | Sequence 1120, Appl1 |
| 38 | 102   | 2.1 | 1176 | 1 | US-10-821-234-897  | Sequence 897, Appl1  |
| 39 | 102   | 2.1 | 3433 | 1 | US-10-714-781A-67  | Sequence 67, Appl1   |
| 40 | 100.5 | 2.1 | 894  | 1 | US-10-485-517-416  | Sequence 416, Appl1  |
| 41 | 100   | 2.1 | 706  | 1 | US-10-485-517-146  | Sequence 146, Appl1  |
| 42 | 99.5  | 2.1 | 482  | 1 | US-10-510-386-48   | Sequence 48, Appl1   |
| 43 | 99.5  | 2.1 | 595  | 1 | US-10-510-386-240  | Sequence 240, Appl1  |
| 44 | 99.5  | 2.1 | 716  | 1 | US-10-131-826A-512 | Sequence 512, Appl1  |
| 45 | 99    | 2.1 | 609  | 7 | US-11-058-555-2    | Sequence 2, Appl1    |

## ALIGNMENTS

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RESULT 1
US-11-013-759-3
; Sequence 3, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Kleid, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; FILE REFERENCE: 1038-921MIS:jd
; CURRENT APPLICATION NUMBER: US/11/013, 759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361, 619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ. ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 3
; LENGTH: 1992
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-3

Query Match          3.9%; Score 187.5; DB 7; length 1992;
Best Local Similarity 19.5%; Pred. No. 5, 1e-05;
Matches 180; Conservative 125; Mismatches 350; Indels 269; Gaps 39;
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QY 41 SCFTPEK---TSATYSLTGD-VFEPFGKGTPLSSCFQTTDNLFLNGHSLTFGFI 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 373 NATTVKVGSSSTTAEILSDSLTFQOPNIGS-----QSTKTVYGVNGVKFT---N 421
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 DATTHGAASATFANKNLPSPGSLSPDSSP-----STVYTGQGLTSAGVN 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 422 NATTAIGTRITTRDKIGFARDGDYDEKAPYLDKKQKVGSAITINDGI---DAQNK 479
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 LENIRKLVAAGNF-----STADGAIKASFLITGSGDALFSNNSSSTKGALA 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 ISLWAGSSANDAVTIEQKAKPTLNAGA--GISVTPFEISVDKSGNVTAPTYNGVK 537
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 TTGCAIANTGTGVRFLSNASTSGAIDEGSISLNKFLYFEGMAATTGCAICNTK 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 538 TT-----ELNSDGS-----DKF-----SVK 553
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 257 ASGSPELISNNKTLIFASVNA-----ETSGGAIHAKKLALS 293
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 554 GSGT-----NNSLVTAETHLASYLEAVNRITDASALQSFVKEEDDDANAITVALDTTK 606
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QY      299  SGGCTEEF-----RNNVSATFKGAGISIDAGSELSTASEGNIIFVNRLLTTSTSDTRK  343
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      607  NAGAVSILKKGKGGVIAIKKQGVY-----FGLSDQSG-LTIGKSTLNNDDITLVKDT  659
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      350  RNAINIGSNG-KFTELPRAKKNHTIFFYDPIITSEGTSDVLKINNGSAGALNPGOITLFS  408
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      660  NEQIOVGANGIKFTNVNGS-----NPGTGIANTARITRDKIGFAGS---GCAVDTN  707
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      409  GETLTADBLKADNLIKSFQTPVSLSGSKLLQKQVTLSESTFSFGSEASLLGMSGTTLS  468
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      708  KPYLDQDQLQVG-NVK-ITNTGINAGSKAITGSLPILPSTADSSRNIEIGNTIQDKK  764
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      469  TTAGSIT-ITVLGINVSLGLKOPVSLTPAKGANKVIVSGKLNLLIDEGNIYESHMFSD  527
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      765  SNAASINDILNTGFNL-----KNNNNDIDFVSTYDIADVFNANGATATVTHD  811
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      528  QLFSLKLTVDADVDYDNDISSLIIPVPAEDPRSEYFGQGGNNVMNTTPTATNTEATATW  587
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      812  TANKTSKVYVNVVD-----DTTHTLTGTDNKKLGVR-----TTKLNTKTSANGN-  856
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      588  TKTGFSVPSPERKSAIVCNLTWGVFDIRSLQOLVEIGATGMEHKGFWVSSMTNTEFLHKTG  647
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      857  TATPNVNVSSBEDALV-----NAQDIENLNTLAKELHTTKGTADTALQITPVYKV  907
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      648  DENRKGFRHTSGGVYIGSSAHTPKDDLFTFAFCHLFARDKCFIAHNSRTYGGTLFFKH  707
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      908  DENNVVA-----DDANAIT-----YQKRNANQVNTLLTKG  937
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      708  SHTL-----QPNVYLTBLGAKPSESAIE-KFP---REIPLADVOVSFSGHS  749
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      938  ENGLANIKTKDKNGTVPFGINTTSGLKAKGSLTNDGSLTKNPGSHQIQVGAD-GYKFAKV  996
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      750  DN-----EMETHYT---SLPSESGSWSNECI-AGGIGLDELPLYLSNHP  789
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      997  NNNGVAGAGIDGTTTRITRDEIGFTGNSLSDSKPHLSKDGINAGKKYI-----  1043
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      790  LKFTIIPQMKYEMVYVSONSPFESSSDRGFSIGRLNLSIPVGAKFPQGDIGDSYTYDL  849
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1046  -----TNIOGGEIAONS-HDAVTGGKTYDLKTELENKISSIAKTAONSILHPSVADE  1096
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      850  SG--FFVSDVYVRNNPOSTATLVMS  871
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1097  QGNNTVSNPVSYSYDTSKTSDVIT  1120
           |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
US-11-013-759-13
; Sequence 13, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS:1b
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 05/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1992
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-13

```

```

QY 4L GCFETPK---TSATYYSLTGP-VFVYRPGKGTPLSDSCFQOTQDNLTFLNDGNSLTFEGFI 96
Db 373 NATTVKVGSSSSSTTAELSDSLFTFOPNTGS-----QSTKYYGVNGVKFT---N 421
QY 97 DAGTHAGAAASTTANKNLTFSGFSLFSDSP-----STTVTGGOTLSAGVN 146
Db 422 NAEFTTAIGTRIRIRIDKIGFARODDVEKQAPYLDKKQKLKGVSAITIDNGI--DAGNKK 479
QY 147 LENIRKLVVGNF-----STADGCAIKGASFLLTGTSQDALFSSNSSSTKGALIA 196
Db 480 ISNIAKSSASADAVTIEQLKAKEPTLNAGA--GISVPTETISYDAKSGNATAPFYNIGVK 537
QY 197 TTAGARIANNTGYVRFLSNIASTSGAIDDEGTSLSNKKFLYFEGNAATTGGALICNTK 256
Db 538 TT-----ELNSDGS---DKF-----SVK 553
QY 257 ASGPELLISNNKTLIPASNYA-----ETSGAIIHAKKLALS 293
Db 554 GSGT-----NSLVTAAEHLASYLEVNRPTADALQSFTVKEEDDDANAIVAKQDTTK 606
QY 294 SGGFTPEFL---KNNVSSAIPKGAIAISIDASGELSLEAFNGNITFVANTLTGTSSTDTPK 349
Db 607 NAGAVSILKIKGKRGKLTIVATKQDQTVT-----FGLSQDSG-LTIGASTLNBDGLTYKDT 659
QY 350 RNAINISNG--KFNELPAAKNHTIFFYDPTISEGTSDVLCINNGSAGALNPYQGTILFS 408
Db 660 NEOIUVGANGIKFTNVGSS-----NPGTGINANTRIIRDTKIGFPGSS---DGAVDTN 707
QY 409 GETTLADELKAADILKKSFTQPVSLSGGKLLQKGVTLTESTSFSGEASLLGMDSGTLLS 468
Db 708 KPYLDODLQYG-NVK--ITNTGINAGGKAITGSLPTLPSIADSSNNIELGNITIDQDK 764
QY 469 TTAGSIT-ITNLGINVDSLGLKQVSLTAKGASKVIVSGKALIDIEGNITYESHMSHD 527
Db 765 SNAASINDIILMTGFNL-----KNNNPIDFVSITYDVIDEPANGATATVTHD 811
QY 528 QLFSLKLTVDADVDPNDVNDISLLIPVPAEDPNSEYFGQGNVNVWTTDTNTKEATATV 587
Db 812 TANKTSKVYVNVND-----DTTILHGTGDNNKGLYK-----TTKLNTKSANGN- 856
QY 588 TKTGVPSPERKSAALVCNTLWGVFTDIRSLQOLVEIGATGMEHKGFVWSMTNPLHKTG 647
Db 857 TATNPNVWSSDEDLV-----NAKDIAENLNTLAKEHTTKGPAADLAQFFYKVV 907
QY 648 DENRGRFHSTGGYVIGGSAHTPYDDELTFEAFCHLPARDKDCFIAHNNSRTYGGTLEFFKH 707
Db 908 DENNNA-----DDANAIT-----VGOKRANNQVNTLLPLKG 937
QY 708 SHTL-----QPNYRLRLGRKSESATL-KP-----REIPLLDVQVSPSHS 749
Db 938 ENGLIKTDKNGVTFEGINTTSGLKAGKSTLNDGLSKNPTGSEQIUVGAD-GVKAAYK 996
QY 750 DN-----RMETHYT-----SLPSESGWSNECT-AGGIGLDPFLVLSNPH 789
Db 997 NNNGVGAGIDGTRIRIRIDELIGFTGTNGSLDKSRPHLSKQINNGKKI-----1045
QY 790 LFKFTIPQMKVEMVYVSONSFSESSSDGRGFSIGRLNLASIPVGAQVQDIDGSIYYDL 849
Db 1046 -----TNIGSGIAQNS-HDAVTGKIDYDLKTELENKISSTAKTAQNLSHFVSAD 1096
QY 850 SG--FVGSVDVYRNNQSTATLYMS 871
Db 1097 QGNNTFVSNPFYSSYDTKSTSDVIT 1120

```

|                       |                   |                    |             |              |
|-----------------------|-------------------|--------------------|-------------|--------------|
| Query Match           | 3.9%;             | Score 187.5;       | DB 7;       | Length 1992; |
| Best Local Similarity | 19.5%;            | Pred. No. 5.1e-05; |             |              |
| Matches 180;          | Conservative 125; | Mismatches 350;    | Indels 265; | Gaps 39      |

RESULT 3  
US-11-013-759-4  
Sequence 4, Application US/11013759  
Publication No. US20050249747A1  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M.  
APPLICANT: Sasaki, Ken  
APPLICANT: Yang, Yan Ping

```

; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN OF MORAXELLA
; FILE REFERENCE: 1038-921MIS-jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2047
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-4

```

```

Query Match      3.9%; Score 187.5; DB 7; Length 2047;
Best Local Similarity 19.5%; Pred. No. 5.3e-05;
Matches 180; Conservative 125; Mismatches 350; Indels 269; Gaps 39;

```

```

Qy 41 SGTFTPK---TSATTYSLTGD-VFYPEPGKPTPLSDSCFQQTDDNLTFLNGHSLTFPGFI 96
Db 428 NATTTVAVGSSSTTALBLSLFTQPTNGS-----QSTSKTYVGNGVKFT---N 476
Qy 97 DAGTHAGAAASTTANKNLTFSGFSLSPDSSP-----STVTYTGQTLSSAGVN 146
Db 477 NAETTAIGTRITRDKIGFARDGDVDEKQAPYLKKQKLVKGSVALITDNGI--DAGNKK 534
Qy 147 LENIRKLVAAGNF-----STADGAIKGASFLLTGTSGDALFSSNSSSTKGGAIA 196
Db 535 ISMLAKSSANDAVTIEQLKAAPKPLNAGA--GISVTPTEISVDKSGNVTAPTYNIGVK 592
Qy 197 TTGARIANNNGYVRFPLSNIASTSGAIDDEGTSILSNKKFLYEGNAATTTGALCNTK 256
Db 593 TT-----ELNSDGTIS---DKF-----SVK 608
Qy 257 ASGSPELIISNNKTLIFASNVA-----ETSGAIIHAKKLALS 293
Db 609 GSGT-----NNSLVTAEHLASYLENVRTADSAIQSTVKEEDDDANAIVAKDTTK 661
Qy 294 SGGTFEFL---RNVSATPKGKAISIDASGELISAETGNITFVRNLTITTTGSTTPK 349
Db 662 NAGAVSILKLKGNKGLVATKKDGTV-----FGLSQDSG-LTIGKSTLNDGLTVKDT 714
Qy 350 RNAINISNG-KFTELRAAKNHTIFVYDPTISEGTSVDVKINNGSAGSLGMDSGTTL 408
Db 715 NEOIQVGANGIKFTYNGS-----NPGTGIANTARITRDKIGFAGS---DGAVDN 762
Qy 409 GETLTADDELKVDNLKSSFTQPVSLSGKLLQKGVLTLESTSFQEGASLIGMDSGTTL 468
Db 763 KPYLDQDKLVG-NVK--ITNTGINAGKAIITGLSPLPLPSIDQSSRNIELGNTIQDKK 819
Qy 469 TTAGSIT-ITNLGINVDSLKQKOPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSD 527
Db 820 SNAASINDIINTGFNL-----KNNNPIDIPVSTYDIDVPANGNATTAATVTHD 866
Qy 528 QLSLKITDADVDVTNVDISLIPVAPDPSSEYGGQGMVNWMTDTATNTKEATATW 587
Db 867 TANKTSRVYDVAND-----DTIHLTGTDNKKLGAVK-----TTKLNTKISAGN- 911
Qy 588 TKTGFPVSPERKALVNCNTLMGVFTDRLSQQLVELIGATGMEHKGQFVWSMTNFLHKTG 647
Db 912 TATNFVNSSDDEDLV-----NAKDIAENNTLAKIHTTKGADRALQTFYVKV 962
Qy 648 DENRKGRRHTSGGVVIGSAHTPKODLFTFAFCHLPARDXOCPIAHNSSTYGGTLFFK 707
Db 963 DENNNA-----DDANAIT-----VGKQANNOVNTTLK 992
Qy 708 SHTL-----QPNYLRIGRAKFSASIR-KFP---RELPLLDVQVVSFS 749
Db 993 ENGLNITKDKNGVTYFGINTTSGLKAKSKSTLNDGSLIKPTGSEQIQVAD-GVFKAKV 1051
Qy 750 DN-----RMEHTYT-----SLPESEGSWSNECI-AGGIGLDLPVLSNPH 789

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Db 1052 NNGGVAGIDGTRITRDEIGFTNGSIDSKSPHLSXQGINAGGKI----- 1100
Qy 790 LFTFTIPQKKEVENVYSSNFFESSDGRGFSIGRLNLTSPVGAKEVQDIDSDTYDL 849
Db 1101 -----TNIOGELIIONS-HDAVGGKIDYDKLELNKISSTAKTAQNSLHESVAD 1151
Qy 850 SG--FPVSDVYRNNPOSTATLYMS 871
Db 1152 QGNFTVSNPYSYDTSKTSDVIT 1175

```

RESULT 4  
US-11-013-759-7

```

; Sequence 7, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.

```

```

; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; FILE REFERENCE: 1038-921MIS-jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: US/09/361,619
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2047
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
; US-11-013-759-7

```

```

Query Match      3.9%; Score 187.5; DB 7; Length 2047;
Best Local Similarity 19.5%; Pred. No. 5.3e-05;
Matches 180; Conservative 125; Mismatches 350; Indels 269; Gaps 39;

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```

Qy 41 SGTFTPK---TSATTYSLTGD-VFYPEPGKPTPLSDSCFQQTDDNLTFLNGHSLTFPGFI 96
Db 428 NATTTVAVGSSSTTALBLSLFTQPTNGS-----QSTSKTYVGNGVKFT---N 476
Qy 97 DAGTHAGAAASTTANKNLTFSGFSLSPDSSP-----STVTYTGQTLSSAGVN 146
Db 477 NAETTAIGTRITRDKIGFARDGDVDEKQAPYLKKQKLVKGSVALITDNGI--DAGNKK 534
Qy 147 LENIRKLVAAGNF-----STADGAIKGASFLLTGTSGDALFSSNSSSTKGGAIA 196
Db 535 ISMLAKSSANDAVTIEQLKAAPKPLNAGA--GISVTPTEISVDKSGNVTAPTYNIGVK 592
Qy 197 TTGARIANNNGYVRFPLSNIASTSGAIDDEGTSILSNKKFLYEGNAATTTGALCNTK 256
Db 593 TT-----ELNSDGTIS---DKF-----SVK 608
Qy 257 ASGSPELIISNNKTLIFASNVA-----ETSGAIIHAKKLALS 293
Db 609 GSGT-----NNSLVTAEHLASYLENVRTADSAIQSTVKEEDDDANAIVAKDTTK 661
Qy 294 SGGTFEFL---RNVSATPKGKAISIDASGELISAETGNITFVRNLTITTTGSTTPK 349
Db 662 NAGAVSILKLKGNKGLVATKKDGTV-----FGLSQDSG-LTIGKSTLNDGLTVKDT 714
Qy 350 RNAINISNG-KFTELRAAKNHTIFVYDPTISEGTSVDVKINNGSAGALNPQGTTL 408
Db 715 NEOIQVGANGIKFTYNGS-----NPGTGIANTARITRDKIGFAGS---DGAVDN 762
Qy 409 GETLTADDELKVDNLKSSFTQPVSLSGKLLQKGVLTLESTSFQEGASLIGMDSGTTL 468
Db 763 KPYLDQDKLVG-NVK--ITNTGINAGKAIITGLSPLPLPSIDQSSRNIELGNTIQDKK 819
Qy 469 TTAGSIT-ITNLGINVDSLKQKOPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSD 527

```

Db 820 SNAASINDILNTGNTL-----KNNNPIDFVSTYDIDVDFANGNATTAATVTHD 866  
Qy 528 QLESLKITVDADVDVNDVNDISLLPVPADPNSEYGOQNNVWTTDTATNTKATATW 587  
Db 867 TANKTSKVVVDVND-----DTYHLTGTTDNKKLGK-----TTKLNKTSANGN- 911  
Qy 588 TKTGFVSPERKSLVLCNLTGWFPTDIRSLQOLVEIGATGMEHKQGFWSMTPLFKTG 647  
Db 912 TATFNNVSSDEDLV-----NAKDINENLTLAKEIHTTKGTADTALQTFYKVV 962  
Qy 648 DENKGRHNSGGYVIGSAHTPKDLETFEAFCHLPARDKDCFIANNSTRYGGTLEFKH 707  
Db 963 DENNNA-----DDNALT-----VGKANNQVNTLTLLKG 992  
Qy 708 SHTL-----QPNYLRLGRAKSESABE-KFP---RELPLADVOVSFHS 749  
Db 993 ENGLINKTKNGVTFGINTTSGLKAKGSTLNDGLSKNPTGSEQIQVGAD-GVKFAKV 1051  
Qy 750 DN-----RMETHYT-----SLPESGSMNECT-AGGIGLDPVLSNPH 789  
Db 1052 NNNVGAGIDGTRITRDELIGFTGTNGSLDKSKPHLSKDGINAGCKI----- 1100  
Qy 790 LFKTFIPQKVMYVYVQNSFFESSSDGRGFSIGRLNLISIPGAKFVQGDIGSYTYDL 849  
Db 1101 -----TNIQGEIAQNS-HDAVTKGKIYDLKTELENKISSTAKTAQNSLHFEVAD 1151  
Qy 850 SG--FVSDVYRANNPQSTATLVMS 871  
Db 1152 QGNFTVSNPYSSYDTSKTSVIT 1175

## RESULT 5

US-11-013-759-9  
; Sequence 9, Application US/11013759  
; Publication No. US20050249747A1  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Sasaki, Ken  
; APPLICANT: Yang, Yan Ping  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
; FILE REFERENCE: 1038-921MIS:1b  
; CURRENT APPLICATION NUMBER: US/11/013,759  
; PRIOR FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: US/09/361,619  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 2053  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
US-11-013-759-9

Query Match 3.6%; Score 172; DB 7; Length 2053;

Best Local Similarity 21.7%; Pred. No. 0.00056;  
Matches 182; Conservative 108; Mismatches 307; Indels 242; Gaps 42;

Qy 42 GTTTPKTSATYSLTGDVFEYEPKGG--TPISDCSFKQTTDNLTFLGNGHSLTFGFLDAG 99  
Db 1209 GLTTPKTLVGNNGNGIYNSQNGNTITGLSNTLANTXK---GSVRTTEQNIKID 1264  
Qy 100 THAGAAAS---TTANKULTTSG-----FSLISFSSPSSTYTTTQCGTLLSAG--- 143  
Db 1265 EDKTRAAASIVDLASGFNLQNGEAVDPEVSTYDTNFANNGNTTAKVYDDTSTKTSKVY 1324  
Qy 144 GVNLENI-----RLVVAAGNFTADG-GAIGKASFLLTGSGDALFSGNS-----SSTKG 192  
Db 1335 DVNVDDTTIEYDKKLGKTKTTLLISTGTGANKFA--LSNQATGDLVLAASDVAHLNLTLS 1382  
Qy 193 GAIAATTAARIANNTGVYRFLSNIASTSGAIDEGTSL--SNNKFLYFEGNAAKTTG 249

Db 1383 GDIQTAKGASQAN-----SAGYVDADDNKVIYDSTDNK--YYQAK-----ND 1423  
Qy 250 GAICNTRKASGPBLIIS-----NNKTLIFASNAVEISGGAIIHAKXLAS-SGGP 297  
Db 1424 GTYDKTRKAVKDXLVQAQTPDGTTLAQMNKVSYNKEQVNDAN-----KKQGINEDNAF 1477  
Qy 298 TEFLRNNVSATPKKGAISIDAGSELSAETGNITFVNLTLLT-----GSTD 346  
Db 1478 VKLEKRAASGNKTKNAAVTV---GDLNAVAQT-PLTFAPDGTGTAKKLGSTLLIKGGQTD 1533  
Qy 347 TPKRANINIG--SNGKFTBLRAKNNHTIFFYDPTISEGTSVYLKIN---NGSGALN 399  
Db 1534 TNLTLNNIGVAVGTGFT-VKLAKDLTNV--NSVAGGFKIDKGIISFVDANGAKAANT 1590  
Qy 400 FYCGTILFSGETTLADELVKADLKSSFPQVPSLSGKLLQGVLTLESTFS-----QE 454  
Db 1591 P-----VLSANGLDL-----GKVISNVGKGTQTDPAANVQLNE 1625  
Qy 455 AGSLGMDSGTTLSTTAGSITI---TNLGINVDSLKQPVSLTAKASN--KVIVSGKL 509  
Db 1626 VRNLLGIGNDMADGNQVNIADIKDPNSGSSSRVTYIKAGTVLGGKGNNDTEKLTATGVQ 1685  
Qy 510 NLIDIRGNIE--SHMF--SHDQFLSKITVDADVDTNVDISLIPVPAE----- 556  
Db 1686 VGVDKDGNANGDLNSVWVTKQDGSKKALATYNAAGQNTNYVTNN---PAEADIRINQ 1741  
Qy 557 -----DPNSEYFGQGNVWTTDTATNTKATATATKGFVSPERKSLVLCNTLM 608  
Db 1742 GIRPFHYNDGNQEPVVOGRNGI---DSASGHSVA---IGFOAKAGEAIV----- 1787  
Qy 609 GVFTDIRSLQOLVEIGATGMEHKQGFWSMTNPLFKTGDE-----NRKGRHNSGGY 661  
Db 1788 -----AIGRQTAQNGQSLAIGNAQTGQSLAIGTGNVAVAGKHSG--- 1828  
Qy 662 VIGGSAHTPKDLETFEAFCHLF--ARDKCFIANNSTRYGGTLEFKHSTLQPOVYLR 719  
Db 1829 AIGDPSTVKADNSYSVGNNGQFTDATQTDVFGVNNI-----TVTESNSVAL 1875  
Qy 720 GRAKFSSEATEKPREIPLADVQVSFSDNEMETHY--TSLPESGSMNECTIAGIG 777  
Db 1876 G---SNSAIS-----AGTHAGTQAKSKDGTAGTTTAAATG 1908

## RESULT 6

US-10-485-517-252  
; Sequence 252, Application US/10485517  
; Publication No. US20050256299A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Sheffield  
; APPLICANT: Biosynexus Incorporated  
; APPLICANT: Foster, Simon  
; APPLICANT: Mond, James  
; TITLE OF INVENTION: Antigenic Polypeptides  
; FILE REFERENCE: PI0629W0  
; CURRENT APPLICATION NUMBER: US/10/485,517  
; PRIOR FILING DATE: 2004-02-02  
; PRIOR APPLICATION NUMBER: GB 0118825.9  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: GB 0200349.9  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 424  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 252  
; LENGTH: 761  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-485-517-252

Query Match 3.6%; Score 171; DB 1; Length 761;

Best Local Similarity 20.0%; Pred. No. 0.00017;  
Matches 106; Conservative 114; Mismatches 232; Indels 78; Gaps 18;



QY 21 QSLANEELSPDDSPFNENIDSGTTPKTS-----ATTYSLTG-----DVFPEPKGTPL 70  
DB 267 QSTQSSESTSTSTLS---DSTSISKSTSQSGSVSTASLSGSESESDSQSSTASBEST 323  
QY 71 SDSGFKQTTNLTFLGNHSLTFEFDAGTHAGAASTANKLTFG--GFGLSFDS 129  
DB 324 SESASTLSDBSTSTNSGSGAST--STLSNSASASEDLSTLSLSTSTASMSQSESDSQ 381  
QY 130 TTVVGGTTLSSAGVNLNIRKLVAAGNFSTADGAI-----KGAFL 173  
DB 382 STASASLSDLSLSTSNMSTASL--STSVSTSESGSTSESTSDSTSTLSLSQSTSR 439  
QY 174 LTGSGDALFSSNNSSTKGAIAITTAARLANNTGYRFLSNIASTSGAIDEGTSL 233  
DB 440 STSASGASTSTSTSDRSTSTASTSMRTSTSDSQMSLSTSTST---MSDSTSLD 495  
QY 234 NNKFLYEGNAAKTTCGAICTKASGSPBELISNNKTLIPASNAVEFGAIAHAKLALS 293  
DB 496 SVSDSTSDSTSTAST-----SGSMVSAISLSDSTSTSTASSEVMSASISDSQMSB 545  
QY 294 SCGFTEFL--RNNVSATPKGAIISIDAGSELST-----AETGNITFVANTLT 342  
DB 546 SVNDSSEVSSESNSSDKSMGSGTSVSDSGSLSTLRKSESVSESSLSGSGSMDSV 605  
QY 343 GSTDTPRRANINIGSNGKFTELRAAKNHTTFYDPT--SEGTSSDVLKINNGSAGALNPY 401  
DB 606 STSDS---SSLSVS-----TSLRSE--SVSESDLSLDSKSTSGSTSTSTSTSTSL 655  
QY 402 QGTILFGEFTLTADLKVAONLKS---SFTQPVLSGGLLKOKVTLLESTFSQAGS 457  
DB 656 SGSESVSESTLSDSISMSDSTSTSDSLSGSISLBSGSLSTSLSDLSKSLLS--SSQS 714  
QY 458 LLMGDSGTTTSTTAGSITITNLGINVDSLGLKOPVSLTAKGASNKVIVSG 507  
DB 715 MSGSESTSTSVSDSQSSSTSNQFDSMSISASESDMSSTSDSS--ISG 761

## RESULT 7

US-11-013-759-11  
; Sequence 11, Application US/11013759  
; Publication No. US20050249747A1  
; GENERAL INFORMATION:  
; APPLICANT: Loosmore, Sheena M.  
; APPLICANT: Sasaki, Ken  
; APPLICANT: Yang, Yan Ping  
; APPLICANT: Klein, Michel H.  
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  
; TITLE OF INVENTION: PROTEIN OF MORAXELLA  
; FILE REFERENCE: 1038-921MIS.Jb  
; CURRENT APPLICATION NUMBER: US/11/013, 759  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: US/09/361, 619  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 2314  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
; US-11-013-759-11

Query Match 3.5%; Score 169.5; DB 7; Length 2314;

Best Local Similarity 20.5%; Pred. No. 0.00096; Mismatches 289; Indels 303; Gaps 40;

Matches 178; Conservative 99; Mismatches 289; Indels 303; Gaps 40;

QY 42 GTTPKTSATTVSYLTGVFPEPKGTPLSDSCFKQTTNLTFLGNHSLTFEFDAGTH 101  
DB 1143 GLTTPKLTGVNNNGKGIIVDSKQNTITG---LSNTLAVNTVDGASHLSQGLAN--DTD 1198  
QY 102 AGAAS---TTANKNLTFSG-----PSLSF--DSSSTVTTTQGLSSAG----- 143  
DB 1199 KTRPASIGDVLANGFNLQNGEAVDFVSTYDVFIDGNATTAKVITDPTSKTSKVYDV 1258

QY 144 -----GVNLNIRKLVAAGN---FSTADGAIKAGASFLTGTSGDALFSN 185  
DB 1259 NVDNKTIETVSDKDLGVKTTTLTKTSANGATKFSAADGDALVKAADIAT----- 1308  
QY 186 NSSSTKGAIAATTAARLANNTGYRFLSNIASTSGAIDEGTSL--SNKFLYEGN 243  
DB 1309 -HUNTLAGDIQTAKGA-----SQASSASAYVADANKYLYDSDTK--KYQVN 1353  
QY 244 AAKTTCGAICTKASGSPBELIS-----NNKTLIPASNAVEFGAIAHAKLAL 292  
DB 1354 ----DKQVDAKKEVAKDKLVAQAQTPDGTLAGMNVKSVINKEQVANDAN-----KQGI 1403  
QY 293 S--SGCFTEFLRNNVSATPKGAIISIDAGSELASAETGNITFVANTLT 342  
DB 1404 NEDNAFIKLENAKDKTKTGNAAVTV---GDLNAAVQT--PLTFAGDTGTAKKLGFTLTI 1459  
QY 343 --GSTDTPRRANINIG--SNGKFTELRAAKNHT-----IFPYD----- 377  
DB 1460 KGGQDTNKLTDNNIGVACTDFT--VKLAKDLTNLSVNAAGTRIDEKGISFVDANGQA 1518  
QY 378 -----ITSEGTSSD-----VLKINNGS--AGALNPY-- 401  
DB 1519 KANTPVLSANGLDLGKRLSNIGAAVDDNDVAVFKQPEVAKTVNNLNQSNAGASLPFV 1578  
QY 402 -----OGT-----ILFSGETL 412  
DB 1579 VTDANGKPIGTGKQKAIKGADEKYHANANGVPEVDKGPITDADKLANTLAHGKPL 1638  
QY 413 TADELKVAD-----NLKSSFTQPVLSGGLLKOKVTLLESTFSQAGSLLGM 461  
DB 1639 DAGHQVVASLGNSDAITLTINIKSTLPQIDTPMTGNANAGQASLSTLSAAQ----- 1691  
QY 462 DSGTTLSTTAGSITITNLGIN-----VDSLGLKQPVSLTAKGASNK 502  
DB 1692 -----SMAASVQDVLANGFNLQTNNOVDPVKAYITVANFVKGTGADITSVRSADGTMSN 1745  
QY 503 VIVSGKLNLDIEGNTY---ESHMFSDQLF---SL--KITVDADVTDVNDISLIPV 553  
DB 1746 ITVNTALAAATDDGAVNLIRAKDGKFKKADDLWNGSLKKGKSASDAKTPGL---SLV-- 1800  
QY 554 PAEDNSEYGFQGC--WNVNMTTDTAINTKATATWTKTGTGVSPERK----- 599  
DB 1801 ---NPNAGKSTDAVALNMLSRAVFKSKDGTITTVSSPDGSIISQGDMSITLSKQGLN 1857  
QY 600 --SALVCNLTLMGV--FVDIRSLQOLVEI-----GATGMEHKQGFWSMTNPLKHTGDN 650  
DB 1858 VGGKVISNKGKGTXTDAAVQQLNEVRNLGLIGNAGNDVADG-----NOVNADIKKDPN 1913  
QY 651 RKGFRTS---GGYVIGSAAHPKDDLFT 676  
DB 1914 SGSSSNRTVYIKAGTVLGKGNNDTEKLAT 1942

## RESULT 8

US-10-485-517-324  
; Sequence 324, Application US/10485517  
; Publication No. US20050256299A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Sheffield  
; APPLICANT: Biosynexus Incorporated  
; APPLICANT: Foster, Simon  
; APPLICANT: Mond, James  
; TITLE OF INVENTION: Antigenic Polypeptides  
; FILE REFERENCE: P100629MO  
; CURRENT APPLICATION NUMBER: US/10/485, 517  
; CURRENT FILING DATE: 2004-02-02  
; PRIOR APPLICATION NUMBER: GB 0118825.9  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: GB 0200349.9  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 424  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 324

LENGTH: 496  
 TYPE: PRT  
 ORGANISM: Staphylococcus aureus  
 US-10-485-517-324

Query Match 3.0%; Score 141.5; DB 1; Length 496;  
 Best Local Similarity 18.8%; Pred. No. 0.0086;  
 Matches 93; Conservative 70; Mismatches 21; Indels 121; Gaps 13;

QY 169 GASFLITGCT-SGDALFSSNNSSSTKGAIATTAGARIANNNGYVFLSNIASTSGAIDDE 227  
 DB 17 GVASVLVGLIGLGLSSKEADASENSVTQSDASNEKSNDSSVSAAPKTDITVSDT 76  
 QY 228 GTSLISNNKFLYFEGNAA--KTTGCAICNTKASGSEPELLISNNKTLIFASNVAETSGAI 285  
 DB 77 KTSNTNNGETSVAQPAQOETTOSSTNATTEETPTGAEATTTTNQANTPATTOSSNT 136  
 QY 286 HAKKALSSGCFEFL-RNNVSATPKGASIDASELSAETGNTTFVRNTLTGGS 344  
 DB 137 NAEELVNOTSNETTFNDTNTVSVNSPQNSTNAE--NVSTQDTSTEAATPSNNEAPOS 193  
 QY 345 TDPFKRNAINIGSNGKFTLELRAKNHTIFFYDPTITSEGTSDVLKINNGSAGALNPYQGT 404  
 DB 194 TDSANKDVNOAVNTSAPRMA-----NVT-----VGIDSG 246  
 QY 405 ILFSGETLTADDELKVAADNLKSSFTQPVLSGSKLLQKGYTLBESTSFQEGSLLGMDSG 464  
 DB 216 --FSLAAVADAPAAAGTDITNQLT-----NVT-----VGIDSG 246  
 QY 465 TTSTAGSITITNLGINVDSLGKQPVSLTAKASNKVYSGKLNLDIEGNIYESHMF 524  
 DB 247 TTVPHQAGYVKLVNPGSPNSAV-----KGDTFKITVPEKELNNGVTSTAKVPPIM 298  
 QY 525 SHDQFLSLKITVDAD-----VDTNVDISLIPVPAE-DPNESEYFGQGMVNT 573  
 DB 299 AGDOV--LANGVIDSDGNVYTFDVTYNTKDVAKALTMPEYIDPE----- 342  
 QY 574 TDTATNTEATATWTKTGFVSPERKSALVNTLMGVFTDIRLQOLVELGATGMEHQG 633  
 DB 343 ----NVKKTGNVTLTGISTTANKTYLVDEYKGYKFNLSIKGTIDQIDKTNNTYRQ- 396  
 QY 634 FWSSMTNPLHKTD 648  
 DB 397 ----TIVNPSGD 405

RESULT 9  
 US-10-485-517-325

Sequence 325, Application US/10485517  
 Publication No. US20050256299A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Sheffield  
 APPLICANT: Biosynex Incorporated  
 APPLICANT: Foster, Simon  
 TITLE OF INVENTION: Antigenic Polypeptides  
 FILE REFERENCE: P100629MO  
 CURRENT APPLICATION NUMBER: US/10/485,517  
 PRIOR FILING DATE: 2004-02-02  
 PRIOR APPLICATION NUMBER: GB 0118825.9  
 PRIOR FILING DATE: 2001-08-02  
 PRIOR APPLICATION NUMBER: GB 0200349.9  
 NUMBER OF SEQ ID NOS: 424  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 325  
 LENGTH: 496  
 TYPE: PRT  
 ORGANISM: Staphylococcus aureus  
 US-10-485-517-325

Query Match 3.0%; Score 141.5; DB 1; Length 496;  
 Best Local Similarity 18.8%; Pred. No. 0.0086;

Matches 93; Conservative 70; Mismatches 21; Indels 121; Gaps 13;

QY 169 GASFLITGCT-SGDALFSSNNSSSTKGAIATTAGARIANNNGYVFLSNIASTSGAIDDE 227  
 DB 17 GVASVLVGLIGLGLSSKEADASENSVTQSDASNEKSNDSSVSAAPKTDITVSDT 76  
 QY 228 GTSLISNNKFLYFEGNAA--KTTGCAICNTKASGSEPELLISNNKTLIFASNVAETSGAI 285  
 DB 77 KTSNTNNGETSVAQPAQOETTOSSTNATTEETPTGAEATTTTNQANTPATTOSSNT 136  
 QY 286 HAKKALSSGCFEFL-RNNVSATPKGASIDASELSAETGNTTFVRNTLTGGS 344  
 DB 137 NAEELVNOTSNETTFNDTNTVSVNSPQNSTNAE--NVSTQDTSTEAATPSNNEAPOS 193  
 QY 345 TDPFKRNAINIGSNGKFTLELRAKNHTIFFYDPTITSEGTSDVLKINNGSAGALNPYQGT 404  
 DB 194 TDSANKDVNOAVNTSAPRMA-----NVT-----VGIDSG 246  
 QY 405 ILFSGETLTADDELKVAADNLKSSFTQPVLSGSKLLQKGYTLBESTSFQEGSLLGMDSG 464  
 DB 216 --FSLAAVADAPAAAGTDITNQLT-----NVT-----VGIDSG 246  
 QY 465 TTSTAGSITITNLGINVDSLGKQPVSLTAKASNKVYSGKLNLDIEGNIYESHMF 524  
 DB 247 TTVPHQAGYVKLVNPGSPNSAV-----KGDTFKITVPEKELNNGVTSTAKVPPIM 298  
 QY 525 SHDQFLSLKITVDAD-----VDTNVDISLIPVPAE-DPNESEYFGQGMVNT 573  
 DB 299 AGDOV--LANGVIDSDGNVYTFDVTYNTKDVAKALTMPEYIDPE----- 342  
 QY 574 TDTATNTEATATWTKTGFVSPERKSALVNTLMGVFTDIRLQOLVELGATGMEHQG 633  
 DB 343 ----NVKKTGNVTLTGISTTANKTYLVDEYKGYKFNLSIKGTIDQIDKTNNTYRQ- 396  
 QY 634 FWSSMTNPLHKTD 648  
 DB 397 ----TIVNPSGD 405

RESULT 10  
 US-10-793-626-1780

Sequence 1780, Application US/10793626  
 Publication No. US20050255478A1  
 GENERAL INFORMATION:  
 APPLICANT: KIMMERLY, WILLIAM JOHN  
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 FILE REFERENCE: P13480US  
 CURRENT APPLICATION NUMBER: US/10/793,626  
 CURRENT FILING DATE: 2004-03-04  
 PRIOR APPLICATION NUMBER: 60/164,258  
 PRIOR FILING DATE: 1999-11-09  
 NUMBER OF SEQ ID NOS: 4472  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 1780  
 LENGTH: 1155  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 OTHER INFORMATION: amino acid sequence  
 US-10-793-626-1780

Query Match 2.9%; Score 140.5; DB 1; Length 1155;  
 Best Local Similarity 22.7%; Pred. No. 0.031;  
 Matches 141; Conservative 72; Mismatches 203; Indels 205; Gaps 35;

QY 33 DSFNGNIDSGT-----FTPKTSATYSLTGVDFYEPKGPPLSDSCRTQTDNLTFL 85  
 DB 581 DSFNPDLNNSNVXDVTSTQFTPKVSA-----DGRPV-DINPARSVAN----- 620  
 QY 86 GNGHSILTFGFLDAG-----THAGAAASTANKXULTFSGFSLSDSSPSTVT-----T 134  
 DB 621 GKXIVVQAVRPTGTGNVYTEYWLTRDGTNTNDFYRG-----TKSTIVYVYVNGSST 672

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Oy 135 GOG-----TSSAGVWLENIKRLV-----VAGNSTADGGAIKASFLITSTGDALFS 184
Db 673 AOGNPFYISLGDYVWLDKKNKGVOODDEKGLAGVYTLKDSNNRELQRYTTOSGHYQD 732
Oy 185 NNSSTKGGAIAATTAGARIANNTRYVRFLSNIASTSGAIDDEGTSILSNKFLYFEGNA 244
Db 723 N-----LQNGTYVWF-----AIPDNYTPSPANN-----756
Oy 245 AKTTGCAI-CNTKASGSPELLISNNKTLIFASNAVETSOGGAIHAKKALSSGGTFELRN 303
Db 757 --STNDADIDSGERGTGRKVVAKK-TINNADNMVTVDGFFYLPK---YVVDY-----804
Oy 304 NVSSATPKGGAISIDASGELSASTAGNTTFPARNLTLTGSDTPKRAININSGNKFT 363
Db 805 -VWEDJNKDG---IODDNEKGIS--NVKYTLKKNKGDTTIGTTTT-----DSNGKY-E 849
Oy 364 LRAAKN--HTIF-----YDPITSEGTSSDVLKINNGSAGALNPYGITLFSGETLTLTD 416
Db 850 FTGLENGDYTLIEFELPEGYTP-TKONSGSDEKDSNG-----TKTYVT 891
Oy 417 LKVADN--LKSFPTQPVLSGGKLL-----LQGYTLBESTSPQOAGSLIGMDS 463
Db 892 VKDADNKRTIDSGFYKPIYNLGDYVWEDTNKXGIDODSEKGISGVAVTLKDKKNMAIG---948
Oy 464 GTTLSTTA-----GSITTI--TNLGINVDSLGIKQPVSLTAKGASKRVIVSGKL 509
Db 949 --TTTTSAGHYQFKLENGSYTVEFEPSPGYTPRKANSQGDITVDSNGITTTTGINGAD 1006
Oy 510 NLIDEGNIYBSHMS-HDQFLSLKITVDADVDOTNVDISLLIPPAEDPNESEYFQG--566
Db 1007 NL-TIDSGFYKTPKXSVGDYWE-----GIDODN-EKGISGVK 1047
Oy 567 -----QNVNMTTDTATNTK 581
Db 1048 VTLKDEKANIISTTTDENGK 1068

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RESULT 11
US-10-510-386-2
Sequence 2, Application US/10510386
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Olsen, Peter Bjørke
APPLICANT: Rasmussen, Michael Dølborg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294,204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 802
TYPE: prt
ORGANISM: Bacillus licheniformis
US-10-510-386-2

```

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Query Match Similarity      2.9%; Score 137.5; DB 1, length 802;
Best Local Similarity       20.8%; Pred. No. 0.03;
Matches 141; Conservative   76; Mismatches 241; Indels 221; Gaps 34

QY    62 YEP-----GKGPPL-SDSCFKQTDTNLLTFELG-----NGHSLTFGFIDAG--THAGA 104
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     136 YKPDSVVRKRDWTLLADATFYPMQMDKSAPRTIGADQAMKSGVTGGIKIVAVIIDSVDYTH-- 192
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    105 AASTTANKLTLFSGFSLLSPDSSPSTTVT-----TSQGT-----              138
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     193 --PDLKNNFGPYKKGYDPVNDYDPEPTFTGDPRGATDHGTHVACTIAANGIKGVAPDEA 250
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY    139 -----LSSAGCVNLLENIRKLIVANG-NFTADGAIGAKASLTLLTGTSGD----- 180

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Db      251 TLIAVVLDPGSGTTE-----VINGIEKAVADGAKWNLSLGNLSNLPDVAITSIALDMA 306
Oy      181 -----ALFSSNSSSTKGCALITTTGARIANTG-----YRFSLNSTASTSGCAI----D 2233
Db      307 MAEGVAVYVNSNGSNGEMNTVSGPOTSRVAISVGSOLPYVEYVUTLPSYSACKMYOE 366
Oy      226 DEGTSILSNKKFLYPE-----GNAAKTTGAI-C-----HTKASGPELI 264
Db      367 EKLEHALNGOEVELVEAGIGADPDSGDVKGAVALORGVIIPVDKAEAKNAKAGALGAV 426
Oy      265 ISNNKTLIFASVVAETSGGAIHAKKALISGGFTEPLENNVSATPKGALISIDASELS 344
Db      427 IYNNATGEIEANY--MGMAVPTVTLKSEEG---EKLVQOI-----KEGKHSVVFSEKLD 4757
Oy      325 LSAETGNIFE-----VRNTLTTTSGTDPRKXNAINISNGKFTLEBLRAKHTTIFVYPI 378
Db      476 KKLGETTAFSSRGRPMQMDTWMIKPDVSA---GNVIVS-----TIPTHDPKN 519
Oy      379 -----TSEGSTDVLKINNGSAGAL-----NPYO--GTILFSGETLT----- 413
Db      520 PYGYSKQGTSMASPRHV-AGTAAILKQAKPMTPEBQIGVLMNTAKULTDENGKPLPHNT 578
Oy      414 --ADELKAVDNLIK-SSFTOPVLSLGGKILLQK-----VTLESTSPQASGILLGMS 463
Db      579 QGAGSRIMEALKASSIVTPGHSYGTELKQKQKOTKQAPFTIINLSHRAAYOLEVSPK 638
Oy      464 GTLTSTTAGSITITNIGINVDSLAKOVPSLTAKGASNKVIVSGKLMJIDIEGNIY--E 520
Db      639 GTGI-IVSGTERVY-----VANOTGAAAKVTVNSAKTAAGTYEGTVIRED 685
Oy      521 SHMFSDQJLSLK-----ITVDADVDTNV-DISSLIPIVPAED----- 557
Db      686 GRKVAEIPILLIIVKEPDYRVTVSVEEGAKQAGATTEIAYIPGAGAEELAFVYDENIMLL 745
Oy      558 -----PNSBYFOG--OWN 569
Db      746 GQAGVTKQKQGYOSTQNM 764

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RESULT 12
US-11-091-643-18
: Sequence 18, Application US/11091643
: Publication No. US20050246789A1
: GENERAL INFORMATION:
: APPLICANT: TANAKA, Masao
: APPLICANT: YOKOYAMA, Tomoko
: APPLICANT: AOYAGI, Moriochi
: APPLICANT: HASEGAWA, Makoto
: APPLICANT: EHARA, Gaku
: APPLICANT: KIMURA, Masaharu
: APPLICANT: NISHIHASHI, Hideji
: TITLE OF INVENTION: Polypeptidic having
: TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
: TITLE OF INVENTION: poynucleotide encoding the same
: FILE REFERENCE: 0P1335
: CURRENT APPLICATION NUMBER: US/11/091,643
: CURRENT FILING DATE: 2005-03-29
: PRIOR APPLICATION NUMBER: JP 2001-115754
: PRIOR FILING DATE: 2001-04-13
: PRIOR APPLICATION NUMBER: JP 2001-203463
: PRIOR FILING DATE: 2001-07-04
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 1332
: TYPE: PRT
: ORGANISM: Bacillus popilliae
US-11-091-643-18

```

|                       |       |              |       |            |     |        |      |
|-----------------------|-------|--------------|-------|------------|-----|--------|------|
| Query Match           | 2.6%  | Score        | 124.5 | DB         | 7   | Length | 1332 |
| Best Local Similarity | 19.0% | Pred. NO.    | 0.43  |            |     |        |      |
| Matches               | 76    | Conservative | 64    | Mismatches | 165 | Indels | 95   |
|                       |       |              |       |            |     | Gaps   | 14   |

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Oy      201 ARLANNQYVRFLSNLSTNGSGAIDDEGHSILNNKFLPYEPGNNAKTTGAI CNTKASGS 260
      330 SRVYIDTGI-----LSTVIGGO-----YNNNNFKRTHYQILRTKTTGGTSFSGSPYIGS 375
Db      261 PELLISNNKTLIFASNVAETSGGAIHAKKALSSGGTFELRNNVASATPKGAI----- 315
      376 TAPFIQRTNLTFGSGDVYTTIESVVRSSL-----YGNASVAFGTTGRSLYENPT 426
Oy      316 -----SIDASGELSLSAETGNITV-----RNTLTGSGTDPKKNAI 353
      427 VYEPAQKLIELHPGVD--SGRPNAVNNSHLSYISGSLGYSPSGGLVYGMTTATAREN 485
Oy      354 NISNGKFTFLRAAKNHTIFPDYPTISEG--TSQVD,KLNNGSAGALNYYQGTILFSGETL 412
Db      486 NITLDDRIVOLPRAVKGASLNNCOVYAGCTFTGCDMLKPNNN--GTFSMY-----FAFRA 538
Oy      413 TADELKADMLKSSFTQPVSLSGK-----LTLQKGVTLESTSFQSEAGSLGMDSGT 465
      539 YTHFRIRRVASNASFSPFVISEBGRPTTTPVLLSTMSPLQNPF--EAKTYVDLSTV 506
Db      466 TLSTTASGITTNLGINVDSLKQPVSLTAKGASNKVIVSGKLLIDIEGNIYE----- 520
Oy      597 TIRTSASATTFQNLNR-----FTVSGSANVLI--DRLEFVPIEBSLFEVETKO 643
Oy      521 -----SHMFSHQDLPSLLKITVDADVDDNNVDSILI 551
Db      644 QLEKARAVNHLFTDGSKALKEDTDTYVIDDPAANVDCI 683

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RESULT 13
US-10-667-295-100
; Sequence 100, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 1196
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1196)
; OTHER INFORMATION: Ceres Seq. ID no. 12653918
US-10-667-295-100

Query Match          2.6%; Score 122; DB 1; Length 1196;
Best Local Similarity 20.4%; Pred. No. 0.54;
Matches 178; Conservative 113; Mismatches 333; Indels 248; Gaps 43

QY      114 LTFSGFSLISFPSSPEPTVTTGQGTLSS-----AGCVNLENIR 151
DB      14 LFFSFFSFSLSPFASPPQSILRYREIHQLISFKDVLDPDKLLPDMSNNKPCTPFDGVTRCDK 73
QY      152 KLIVAGNFSTAOGAIKGASFLLTGTSGDALFSNNSS-----SSTKGCAIATTAGARIAN 205
DB      74 VTSIDLSSPLNVGFPAVSSLSLTGLGESLPFLSNHINOSVGFCPSLHSIDLSTRNS 133
QY      206 NTGYVRFLSNIASTSGCALIDEGFTSLSNKKPLFYEGNAAKTTGGAI CNTRKASGPDLII 265
DB      134 LSGPVTTTLTSLSCSG-----LKPLNVASN----- 158
QY      266 SNNKTLLIPASNVAVETGGCAIHAKKLALSSCGFTPELRNVVSSATTPKGCALSIDAGSEL 325
DB      159 ----TLDFPGKV---SGG-----LRLNISLEVLDISANSISGANVVGWALS -DGGCELKH 204

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QY 326 SAEGNITFRNLTLTGGTDTPK---NNAINISNGKFTLRAKKNHTTFYFPIRSEG 382
Dd 205 LAISGN-----KISGDVDSRCVNLNLFIDVSSNNRSTGI-----PFLGDC 244
QY 383 TSSDVLKINNGSAGALNPYQGTILLTSGGTTLPADELKADNLKSFQTPV----- 411
Dd 245 SAQOHLDISG-----NKLSDG--FSRAISCTEKLKLNISNPFVGPBPPLPLKLOYL 286
QY 432 SLISGKLLLOKQVLTLESTSF--SQBAGSLIGMD--SGT-----TLSTAGSIT--ITVLGINVD 484
Dd 297 SLLENKF-----TGEIPDPLSGACDTLTGLDLSNHHYGAVPFPFSGCSLSEBALSN 350
QY 485 SLGKOPVSLTAKGASNKVYISGKLNLDIEGNIYESHMFSDQLFSLIKITYDADVDN 544
Dd 351 NFGSELPMQDILKMRGLKVL---DISFNEFSGELPES-----LTMLSASILTLDLSSN 400
QY 545 VDISLILPFAEDPNP-----EYQOGQGNVNVMTDTATNKKEATMTK---TGF 592
Dd 401 NFGSPILPMLCONPKNTLOELYLONNGFTGK---IPPLTSLNCSLWLSHLSTNYLSGT 455
QY 593 VP-----SPERSALVCNTLNGVFTD---IRSLQOLV-----EIGATGMEHQGF 634
Dd 456 IPSLSGLSLKRLPKLMLNMLEGELPQELMAYKTELTETILDPNDLTGEI--PSGLSNTNL 514
QY 635 -WWSMTNPLAKTGD-----ENRKGFRTSGGYVIGGSAHTPKDILFTFAFCHLFAR 665
Dd 515 NMWISLNNRL--TGEIPKWIGRLLENALIKLSNNSF--SGNIPALBGCRSLIWLDI--- 567
QY 686 DKDCFIANNNSRYTGGT---FFKSHITLOPNYIRLORARF--SESALEKPRRPIALD 744
Dd 568 -----NTNLFNCTIIPAMFKQSGKI--AANFIAGRRVYIINKDGKKECHGAGNLE 617
QY 742 VQVFSHSDRMETHTYSLPSESGSNEC-----IAGGIGLDLPVLSNHPPLFKTFIP 796
Dd 618 FQGRSGLNRLSTR-----NPNCTITSRYGG-----HNSPFIDNGS 655
QY 797 QMKVEWYYSQNSFPSSSDGFGSISGRLLNISIPVGAKFVQGDIGDSYTYDLSGFVSD 856
Dd 656 MMFLMDKYNMNLGYIPEKIGSMPYLF--ILNL-----GHNDISGISPDE--VQDLGLGNILD 708
QY 857 VYRRN-----POSTATLNSPDSWKIRGNGLS 883
Dd 709 LSSNKLDGRIPQAMSAIWLWTEL--DLSNNLS 739

```

```

RESULT 14
US-11-074-176-12
; Sequence 12, Application US/11074176
; Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAuliffe, Olivia
APPLICANT: Perill, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 391
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 457
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
US-11-074-176-12

Query Match          2.5%; Score 119.5; DB 7; Length 457,
Best Local Similarity 19.7%; Pred. No. 0.22;

```



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: November 25, 2005, 14:20:23 ; Search time 108.724 Seconds  
(without alignments)  
3750.264 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 928  
Sequence: 1 MKTSIPWLVSSVLAFFSCHL.....MELRGSSRMVNVDTKLRP 928

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_21.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*  
9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 928   | 100.0       | 928    | 2  | AAW88417 Chlamydia   |
| 2          | 928   | 100.0       | 928    | 3  | AAW88417 Chlamydia   |
| 3          | 928   | 100.0       | 928    | 5  | ABW90583 Chlamydia   |
| 4          | 928   | 100.0       | 928    | 6  | ABW90583 Chlamydia   |
| 5          | 827   | 89.1        | 949    | 2  | AAW35060 Chlamydia   |
| 6          | 12    | 1.3         | 230    | 2  | AAW34612 Chlamydia   |
| 7          | 12    | 1.3         | 746    | 5  | ABW90535 Chlamydia   |
| 8          | 12    | 1.3         | 928    | 3  | AAW88421 Chlamydia   |
| 9          | 12    | 1.3         | 928    | 3  | AAW94327 Chlamydia   |
| 10         | 10    | 1.1         | 10     | 7  | ADW30988 HLA bindi   |
| 11         | 10    | 1.1         | 10     | 7  | ADW30926 HLA bindi   |
| 12         | 10    | 1.1         | 10     | 7  | ADW30940 HLA bindi   |
| 13         | 10    | 1.1         | 395    | 5  | ABW90536 Chlamydia   |
| 14         | 10    | 1.1         | 450    | 5  | AAW34617 Chlamydia   |
| 15         | 10    | 1.1         | 839    | 5  | ABW56002 Chlamydia   |
| 16         | 10    | 1.1         | 839    | 5  | ABW98211 Chlamydia   |
| 17         | 10    | 1.1         | 839    | 6  | ABW62627 C. psittaci |
| 18         | 10    | 1.1         | 945    | 2  | AAW88428 Chlamydia   |
| 19         | 10    | 1.1         | 945    | 3  | AAW63368 Amino aci   |
| 20         | 9     | 1.0         | 9      | 7  | ADW30943 HLA bindi   |
| 21         | 9     | 1.0         | 930    | 2  | AAW88424 Chlamydia   |
| 22         | 9     | 1.0         | 930    | 2  | AAW35052 Chlamydia   |
| 23         | 9     | 1.0         | 930    | 5  | AAW90240 Chlamydia   |
| 24         | 9     | 1.0         | 930    | 5  | ABW90548 Chlamydia   |

|    |   |     |     |   |                    |
|----|---|-----|-----|---|--------------------|
| 25 | 9 | 1.0 | 930 | 6 | ABW26756 Protein e |
| 26 | 8 | 0.9 | 76  | 8 | ADK48420 Streptoco |
| 27 | 8 | 0.9 | 76  | 8 | ADR94994 Novel S.  |
| 28 | 8 | 0.9 | 76  | 9 | AEA58864 Streptoco |
| 29 | 8 | 0.9 | 93  | 4 | AAU14380 Human nov |
| 30 | 8 | 0.9 | 93  | 4 | AAU14144 Human nov |
| 31 | 8 | 0.9 | 93  | 8 | ADH80698 Human pol |
| 32 | 8 | 0.9 | 112 | 4 | AAW74946 Human col |
| 33 | 8 | 0.9 | 199 | 8 | ADL05508 M. catarr |
| 34 | 8 | 0.9 | 218 | 3 | AAW95842 Maize hea |
| 35 | 8 | 0.9 | 218 | 4 | AAW82764 Maize hea |
| 36 | 8 | 0.9 | 218 | 7 | ABU10034 Maize mlt |
| 37 | 8 | 0.9 | 218 | 8 | ADM48273 Polypepti |
| 38 | 8 | 0.9 | 227 | 8 | ADH51632 Novel cen |
| 39 | 8 | 0.9 | 234 | 4 | AAW87249 Novel hum |
| 40 | 8 | 0.9 | 234 | 8 | ADL54564 Novel hum |
| 41 | 8 | 0.9 | 251 | 7 | ADP59589 Human pol |
| 42 | 8 | 0.9 | 267 | 4 | AAU19709 Human nov |
| 43 | 8 | 0.9 | 267 | 5 | ABP47929 Human pol |
| 44 | 8 | 0.9 | 267 | 7 | ADC10891 Human ext |
| 45 | 8 | 0.9 | 312 | 8 | ADY12178 Plant ful |

## ALIGNMENTS

RESULT 1.  
ID AAW88417 standard, protein, 928 AA.  
AC AAW88417;  
XX  
DT 17-OCT-2003 (revised)  
DT 26-APR-1999 (first entry)  
XX  
DE Chlamydia pneumoniae surface exposed protein Omp4.  
XX  
KM Omp4, outer membrane protein 4; surface exposed protein; antigen;  
infection; diagnosis; vaccine; atherosclerosis; asthma.  
XX  
OS Chlamydia pneumoniae.  
XX  
PN W09858953-A2.  
XX  
PD 30-DEC-1998.  
XX  
PF 19-JUN-1998; 98WC-DK000266.  
XX  
PR 23-JUN-1997; 97DK-0000744.  
XX  
PA (BIRK/) BIRKELUND S.  
PA (CHR/) CHRISTIANSEN G.  
XX  
PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;  
WPI: 1999-105610/09.  
XX  
DR N-PSDB; AAX06816.  
XX  
PT Species-specific test for identifying mammals infected with Chlamydia  
pneumoniae - comprises detecting antibodies specific for outer membrane  
proteins of C. pneumoniae or nucleic acids encoding these proteins.  
XX  
PS Claim 7; Page 40-42; 115pp; English.  
XX  
CC This polypeptide comprises the novel 98.9 kDa surface exposed protein  
Omp4 of the human respiratory pathogen Chlamydia pneumoniae. Its amino  
acid sequence was deduced from DNA (see AAX06816) isolated from a C.  
pneumoniae expression library. The invention provides 12 novel surface  
exposed proteins, Omp4-Omps (see AAW88417-28), and nucleic acid  
sequences encoding them (see AAX06816-27). A new species specific test is  
claimed that is used to identify mammals (including humans) infected with  
Chlamydia pneumoniae. The test comprises detecting antibodies specific  
for Omp4-Omps or detecting nucleic acid fragments encoding these outer





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QY 1 MKTSLPWLVSVLAFSCHLQSLANBELLSPPDSFNGNIDSGTFPTKTSATYSLTGDFV 60
DB 1 MKTSLPWLVSVLAFSCHLQSLANBELLSPPDSFNGNIDSGTFPTKTSATYSLTGDFV 60
QY 61 FYRPGKTPSLDSCFKQKTNDNLTFGLNGHSLTFGFLDAGTHAGAASTTANKULTFSGFS 120
DB 61 FYRPGKTPSLDSCFKQKTNDNLTFGLNGHSLTFGFLDAGTHAGAASTTANKULTFSGFS 120
QY 121 LLSFDDSPSTVTYTGQGLSSAGVNLNRLKLVNAGNFTAGGAIKKSAPLLTGTSGD 180
DB 121 LLSFDDSPSTVTYTGQGLSSAGVNLNRLKLVNAGNFTAGGAIKKSAPLLTGTSGD 180
QY 181 ALFSNNSSSTKGGAIATTAGARIANNNGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
DB 181 ALFSNNSSSTKGGAIATTAGARIANNNGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAKTTGGALCNTKASGSPPELLISNNKTLIFASNAETSGAIIHAKKLALSSGGFTEF 300
DB 241 EGNAAKTTGGALCNTKASGSPPELLISNNKTLIFASNAETSGAIIHAKKLALSSGGFTEF 300
QY 301 LRNNVSATPKGAIISTDASGELSLAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 360
DB 301 LRNNVSATPKGAIISTDASGELSLAETGNITFVRNTLTGTSSTDPKRNAINIGSNGK 360
QY 361 FTELRAKNTTIFPYDPTSEGTSDVLKINNAGALNPYOGTILFSGEFLTADELKVA 420
DB 361 FTELRAKNTTIFPYDPTSEGTSDVLKINNAGALNPYOGTILFSGEFLTADELKVA 420
QY 421 DNLKSFPTQVSLSGCKLLQKGVLTSTSPSOBAGSLLMDSGTLSTTAGSIITTNLG 480
DB 421 DNLKSFPTQVSLSGCKLLQKGVLTSTSPSOBAGSLLMDSGTLSTTAGSIITTNLG 480
QY 481 INVDSLGLKQPVSLTAKGANKYIVSGKLLIDIEGIVSHMFSDHQLFSLLKITVDAD 540
DB 481 INVDSLGLKQPVSLTAKGANKYIVSGKLLIDIEGIVSHMFSDHQLFSLLKITVDAD 540
QY 541 VDTNVDISLIPYADPNSEYGFQOGMNVMTTDTATNTKEATATWTKTGPVSPERKS 600
DB 541 VDTNVDISLIPYADPNSEYGFQOGMNVMTTDTATNTKEATATWTKTGPVSPERKS 600
QY 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVSSMTNPLHKTGDENRKGFRTSGG 660
DB 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQGFVSSMTNPLHKTGDENRKGFRTSGG 660
QY 661 YVIGGSAHTPKDULFTFAFCHLPARDKCFIAHNNSTRTYGTLPFKHSHTLQPNYLRIG 720
DB 661 YVIGGSAHTPKDULFTFAFCHLPARDKCFIAHNNSTRTYGTLPFKHSHTLQPNYLRIG 720
QY 721 RAKPSESATKPREIPLALDVQVSPSHDNRMETHYTSLPESFGSMNSNCIAGGIGLDL 780
DB 721 RAKPSESATKPREIPLALDVQVSPSHDNRMETHYTSLPESFGSMNSNCIAGGIGLDL 780
QY 781 PFVLSNHPLEFKTFIPQMKVEMVYVQNSFEFSSSDRGFSIGRLNLSPVGAKEVQGD 840
DB 781 PFVLSNHPLEFKTFIPQMKVEMVYVQNSFEFSSSDRGFSIGRLNLSPVGAKEVQGD 840
QY 841 IGSYTYDLSGFVSDVYRNNPOSTATLWMSPDWKIRGNLSBOAFLRGNNYVYNSN 900
DB 841 IGSYTYDLSGFVSDVYRNNPOSTATLWMSPDWKIRGNLSBOAFLRGNNYVYNSN 900
QY 901 CELFGHAMELRGSSRYNVDVGTKLRF 928
DB 901 CELFGHAMELRGSSRYNVDVGTKLRF 928

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RESULT 3
ABB90583
ID ABB90583 standard; protein: 928 AA.
AC ABB90583;
XX
DT 29-AUG-2003 (revised)

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DT 29-JUL-2002 (first entry)
XX Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
DE Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
XX Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
KW Chlamydia pneumoniae cp6733 protein, SEQ ID NO:115.
KW human respiratory disease; cardiovascular disease; atherosclerosis;
KW coronary artery disease; carotid artery stenosis; myocardial infarction;
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW strain CML029.
XX Chlamydia pneumoniae.
OS Chlamydia pneumoniae.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein /label= Signal_peptide
FT 18..928
FT /note= "mature protein"
XX
PN MO200202606-A2.
XX
PD 10-JAN-2002.
XX
PF 03-JUL-2001; 2001WO-1B001445.
XX
PR 03-JUL-2000; 2000GB-00016363.
PR 11-JUL-2000; 2000GB-00017047.
PR 21-JUL-2000; 2000GB-00017983.
PR 07-AUG-2000; 2000GB-00019368.
PR 18-AUG-2000; 2000GB-00020440.
PR 14-SEP-2000; 2000GB-00022583.
PR 10-NOV-2000; 2000GB-00027549.
PR 22-DEC-2000; 2000GB-00031706.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Ratti G, Grandi G;
XX
DR N-PSDB; ABL91241.
XX
WP1; 2002-154726/20.
XX
DR N-PSDB; ABL91241.
XX
PT Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX
PS Claim 1; Page 96-97; 364pp; English.
XX
XX Sequences ABB90583-ABB90715 represent novel proteins from Chlamydia
XX pneumoniae (strain CML029), and ABL91184-ABL91373 represent DNA encoding
XX them. The proteins are predicted to be immunogenic and may therefore be
XX useful in vaccine production and for diagnostic purposes. Chlamydia
XX pneumoniae is a common cause of respiratory disease in humans, and is
XX also involved in the development of cardiovascular diseases such as
XX atherosclerosis, coronary artery disease, carotid artery stenosis,
XX myocardial infarction, cerebrovascular disease, aortic aneurysm,
XX claudication and stroke. The proteins and nucleic acids of the invention
XX may be used in vaccines and pharmaceutical compositions for the
XX prevention or treatment of chlamydial infections, particularly Chlamydia
XX pneumoniae infections. The proteins may also be used in the detection of
XX Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
XX DNA probe assay or blotting techniques for determining Chlamydia
XX pneumoniae gene expression. The present sequence represents a
XX specifically claimed Chlamydia pneumoniae protein of the invention.
XX (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 928 AA;

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Query Match 100.0%; Score 928; DB 5; Length 928;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKTSLPWLVSVLAFSCHLQSLANBELLSPPDSFNGNIDSGTFPTKTSATYSLTGDFV 60
DB 1 MKTSLPWLVSVLAFSCHLQSLANBELLSPPDSFNGNIDSGTFPTKTSATYSLTGDFV 60

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QY 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIIDAGTHAGAAASTANKULTFS9GFS 120
DB 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIIDAGTHAGAAASTANKULTFS9GFS 120
QY 121 LLSFDSSPSTVTYTTGGTSLSSAGVNLNIRKLVVAANFSTAGGAIKAGSFLITGSGD 180
DB 121 LLSFDSSPSTVTYTTGGTSLSSAGVNLNIRKLVVAANFSTAGGAIKAGSFLITGSGD 180
QY 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
DB 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAKTGGAI CNTKASGSPBELLISNNKTLIFASVAETSGAIIHAKKLALSSGGFTTF 300
DB 241 EGNAAKTGGAI CNTKASGSPBELLISNNKTLIFASVAETSGAIIHAKKLALSSGGFTTF 300
QY 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGSGTDPKRNAINIGSNGK 360
DB 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGSGTDPKRNAINIGSNGK 360
QY 361 FTFLRAAKNHTIFFYDPIITSEGTSDVLKINNAGALNPYOGTILFSGETTLTADELKVA 420
DB 361 FTFLRAAKNHTIFFYDPIITSEGTSDVLKINNAGALNPYOGTILFSGETTLTADELKVA 420
QY 421 DNIKSSFTQPVSLSGKLLQKGVLTLESTFSQDAGSLGMDSGTTLSTAGSITITNLG 480
DB 421 DNIKSSFTQPVSLSGKLLQKGVLTLESTFSQDAGSLGMDSGTTLSTAGSITITNLG 480
QY 481 INVDSLGKQPVSLTAKGASNKYIVSGKLNIDIEGVIYSNMFSDQLFSLKITVDAD 540
DB 481 INVDSLGKQPVSLTAKGASNKYIVSGKLNIDIEGVIYSNMFSDQLFSLKITVDAD 540
QY 541 VDNVNDISLIPVPAEDPNSEYGFQGOVMNMTTDTATNKATATWTKGFVSPERKS 600
DB 541 VDNVNDISLIPVPAEDPNSEYGFQGOVMNMTTDTATNKATATWTKGFVSPERKS 600
QY 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDENRKGFRHTSG 660
DB 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDENRKGFRHTSG 660
QY 661 YVIGGSAHTPKDILFTFAFCHLPARDKCTIAHNSSTTYGTLFFKASHLQONTYRLG 720
DB 661 YVIGGSAHTPKDILFTFAFCHLPARDKCTIAHNSSTTYGTLFFKASHLQONTYRLG 720
QY 721 RAKPSESATKEKPEIPLALDVQVFSHSDNRMEHTHTSLPESRGSNSNCTIAGIGLDL 780
DB 721 RAKPSESATKEKPEIPLALDVQVFSHSDNRMEHTHTSLPESRGSNSNCTIAGIGLDL 780
QY 781 PFVLSNHPLEKTFIIPQKVMYVVSQNSFESSSDRGFSIGRLNLISIPGAKEVQGD 840
DB 781 PFVLSNHPLEKTFIIPQKVMYVVSQNSFESSSDRGFSIGRLNLISIPGAKEVQGD 840
QY 841 IGDSTYDLSGFVSDVYRNNPOSTATLVSPDSWKIRGNLSRQAFLLRGSNNYVNSN 900
DB 841 IGDSTYDLSGFVSDVYRNNPOSTATLVSPDSWKIRGNLSRQAFLLRGSNNYVNSN 900
QY 901 CELFGHAMELRGSSRYNVDVGTCLRF 928
DB 901 CELFGHAMELRGSSRYNVDVGTCLRF 928

RESULT 5
ID AAY35060 standard; protein: 949 AA.
AC AAY35060;
XX 17-OCT-2003 (revised)
XX 13-SEP-1999 (first entry)
DE Chlamydia pneumoniae cellular envelope protein.
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
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KW sinuinitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope.
OS Chlamydia pneumoniae.
EN MO9927105-A2.
PD 03-JUN-1999.
XX 20-NOV-1998; 98MO-1B001890.
PF 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 980S-0107078P.
XX (GEST ) GENSET.
PA
XX Griffais R;
XX WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae.
PS Page 947-949; Disclosure: 1912pp; English.
XX
CC AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAY91990) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 949 AA;
Query Match 89.1%; Score 827; DB 2; Length 949;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKTSLPVLVSSVLAFSCHLQSLANEELSPDSEFNGNIDSGTFPPTKSATYSLTGDF 60
DB 22 MKTSLPVLVSSVLAFSCHLQSLANEELSPDSEFNGNIDSGTFPPTKSATYSLTGDF 81
QY 61 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIIDAGTHAGAAASTANKULTFS9GFS 120
DB 82 FYEPGKGTPLSDSCFKQTTDNLTFLGNGHSLTFGFIIDAGTHAGAAASTANKULTFS9GFS 141
QY 121 LLSFDSSPSTVTYTTGGTSLSSAGVNLNIRKLVVAANFSTAGGAIKAGSFLITGSGD 180
DB 142 LLSFDSSPSTVTYTTGGTSLSSAGVNLNIRKLVVAANFSTAGGAIKAGSFLITGSGD 201
QY 181 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 240
DB 202 ALFSNNSSSTKGAIAATTAGARIANNTGYRFLSNIASTSGAIDDEGTSILSNKFLYF 261
QY 241 EGNAAKTGGAI CNTKASGSPBELLISNNKTLIFASVAETSGAIIHAKKLALSSGGFTTF 300
DB 262 EGNAAKTGGAI CNTKASGSPBELLISNNKTLIFASVAETSGAIIHAKKLALSSGGFTTF 321
QY 301 LRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGSGTDPKRNAINIGSNGK 360
DB 322 LRNNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGSGTDPKRNAINIGSNGK 381
QY 361 FTFLRAAKNHTIFFYDPIITSEGTSDVLKINNAGALNPYOGTILFSGETTLTADELKVA 420
DB 382 FTFLRAAKNHTIFFYDPIITSEGTSDVLKINNAGALNPYOGTILFSGETTLTADELKVA 441
QY 421 DNIKSSFTQPVSLSGKLLQKGVLTLESTFSQDAGSLGMDSGTTLSTAGSITITNLG 480
DB 442 DNIKSSFTQPVSLSGKLLQKGVLTLESTFSQDAGSLGMDSGTTLSTAGSITITNLG 501
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QY 481 INVDSLGIKQPVSTLAKGASNKVIVSGKLNIDIEGNIYESHMFSDQLFSLKITYDAD 540
DB 502 INVDSLGIKQPVSTLAKGASNKVIVSGKLNIDIEGNIYESHMFSDQLFSLKITYDAD 561
QY 541 VDTNVDISSLIPVAEDPNSIEYFGQGMNVMTTDTATNTKEATATWTGTGFPVSPERKS 600
DB 562 VDTNVDISSLIPVAEDPNSIEYFGQGMNVMTTDTATNTKEATATWTGTGFPVSPERKS 621
QY 601 ALVGNLTLMGVFTDRLSLQQLVEIGATGMEHKQGFVWSMTNPLFKTGDENKGRFHTSGG 660
DB 622 ALVGNLTLMGVFTDRLSLQQLVEIGATGMEHKQGFVWSMTNPLFKTGDENKGRFHTSGG 681
QY 661 YVIGSATTPKODLFTFAFCHLFARDKDCFTAHNNSRTYGGTLFPKSHHTLQPNYLRIG 720
DB 682 YVIGSATTPKODLFTFAFCHLFARDKDCFTAHNNSRTYGGTLFPKSHHTLQPNYLRIG 741
QY 721 RAKFSESAIEKFPREIPLALDVQVSFHSNDRMETHYLSLPESSGSNNECIAIGIGIDL 780
DB 742 RAKFSESAIEKFPREIPLALDVQVSFHSNDRMETHYLSLPESSGSNNECIAIGIGIDL 801
QY 781 PFVLSNPHPLFKTFIPQMKVEMVYVYVSONSFESSSDGSGFISGRLLNLSTIPVGAKFVQGD 840
DB 802 PFVLSNPHPLFKTFIPQMKVEMVYVYVSONSFESSSDGSGFISGRLLNLSTIPVGAKFVQGD 861
QY 841 IGDSTYTYDLSGFPVSDVYRNPNPOSTATLLWMSPDSSWKLIRGNLSRQAFLLRGSNNVYVNSN 900
DB 862 IGDSTYTYDLSGFPVSDVYRNPNPOSTATLLWMSPDSSWKLIRGNLSRQAFLLRGSNNVYVNSN 921
QY 901 CELFGHYAMELRGSSRRNPNVDVGTKLRF 928
DB 922 CELFGHYAMELRGSSRRNPNVDVGTKLRF 949

RESULT 6
AAV34612
ID AAV34612 standard; protein; 230 AA.
AC AAV34612;
XX
XX 17-OCT-2003 (revised)
DT 13-SEP-1999 (first entry)
XX
XX Chlamydia pneumoniae transmembrane protein sequence.
DE
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KM neutralising epitope.
XX
XX Chlamydia pneumoniae.
OS
XX MO9927105-A2.
PN
XX 03-JUN-1999.
PD
XX 20-NOV-1998; 98WO-1B001890.
PF
XX 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
XX (GSEST ) GENSET.
PA
XX Grifffais R;
PI
XX WPI, 1999-357842/30.
DR
XX
XX Genome sequence of Chlamydia pneumoniae.
PT
XX Page 633; Disclosure; 1912pp; English.
PS
XX AAV34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAV31990) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis

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CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAV34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 230 AA;
Query Match 1.3%; Score 12; DB 2; Length 230;
Best Local Similarity 100.0%; Pred.No. 0.019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 910 ELRGSSRRNPNVD 921
DB 212 ELRGSSRRNPNVD 223

RESULT 7
ABB90535
ID ABB90535 standard; protein; 746 AA.
AC ABB90535;
XX
XX 29-AUG-2003 (revised)
DT 29-JUL-2002 (first entry)
XX
DE Chlamydia pneumoniae cp0015 protein, SEQ ID NO:19.
XX
XX Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KM human respiratory disease; cardiovascular disease; atherosclerosis;
KM coronary artery disease; carotid artery stenosis; myocardial infarction;
KM cerebrovascular disease; aortic aneurysm; claudication; stroke;
KM strain CWL029.
XX
XX Chlamydia pneumoniae.
OS
XX MO200202606-A2.
PN
XX 10-JAN-2002.
PD
XX
XX 03-JUL-2001; 2001WO-1B001445.
PF
XX
XX 03-JUL-2000; 2000GB-00016363.
PR 11-JUL-2000; 2000GB-00017047.
XX 21-JUL-2000; 2000GB-00017983.
PR 07-AUG-2000; 2000GB-00019368.
XX 18-AUG-2000; 2000GB-00020440.
PR 14-SEP-2000; 2000GB-00022583.
XX 10-NOV-2000; 2000GB-00027549.
PR 22-DEC-2000; 2000GB-00031706.
XX
XX (CHIR-) CHIRON SPA.
PA
XX Ratti G, Grandi G;
PI
XX WPI: 2002-154726/20.
DR N-PSDB; ABL91193.
XX
XX Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT medicament for treatment or prevention of infection due to Chlamydia,
PT preferably Chlamydia pneumoniae, and for diagnostic purposes.
XX
XX Claim 1; Page 49-50; 364pp; English.
PS
XX
XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC them. The proteins are predicted to be immunogenic and may therefore be
CC useful in vaccine production and for diagnostic purposes. Chlamydia
CC pneumoniae is a common cause of respiratory disease in humans, and is
CC also involved in the development of cardiovascular diseases such as

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CC atherosclerosis, coronary artery disease, carotid artery stenosis,  
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,  
 CC claudication and stroke. The proteins and nucleic acids of the invention  
 CC may be used in vaccines and pharmaceutical compositions for the  
 CC prevention or treatment of chlamydial infections, particularly Chlamydia  
 CC pneumoniae infections. The proteins may also be used in the detection of  
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched  
 CC DNA probe assay or blotting techniques for determining Chlamydia  
 CC pneumoniae gene expression. The present sequence represents a  
 CC specifically claimed Chlamydia pneumoniae protein of the invention.  
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 746 AA;

QY Query Match 1.3%; Score 12; DB 5; Length 746;  
 Best Local Similarity 100.0%; Pred. No. 0.056;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 910 ELRGSSRNRYND 921  
 |||||  
 728 ELRGSSRNRYND 739

RESULT 8  
 AAW88421

ID AAW88421 standard; protein; 928 AA.

XX AAW88421;

DT 17-OCT-2003 (revised)

DT 26-APR-1999 (first entry)

XX Chlamydia pneumoniae surface exposed protein Omp8.

KM Omp8; outer membrane protein 8; surface exposed protein; antigen;  
 infection; diagnosis; vaccine; atherosclerosis; asthma.

XX Chlamydia pneumoniae.

PN WO958953-A2.

PD 30-DEC-1998.

PF 19-JUN-1998; 98MO-DK000266.

PR 23-JUN-1997; 97DK-00000744.

PA (BIRK/) BIRKELUND S.

PA (CHRI/) CHRISTIANSEN G.

PI Birkelund S, Christiansen G, Knudsen K, Madsen A, Mygind P;

DR WPI; 1999-105610/09.

DR N-PSDB; AAX06820.

PT Species-specific test for identifying mammals infected with Chlamydia  
 pneumoniae - comprises detecting antibodies specific for outer membrane  
 PT proteins of C. pneumoniae or nucleic acids encoding these proteins.

PS Claim 7; Page 53-55; 115pp; English.

XX This polypeptide comprises the novel 90.0 kDa surface exposed protein  
 CC Omp8 of the human respiratory pathogen Chlamydia pneumoniae. Its amino  
 CC acid sequence was deduced from DNA (see AAX06820) isolated from a C.  
 CC pneumoniae expression library. The invention provides 12 novel surface  
 CC exposed proteins, Omp4-Omp15 (see AAW88417-28), and nucleic acid  
 CC sequences encoding them (see AAX06816-27). A new species specific test is  
 CC claimed that is used to identify mammals (including humans) infected with  
 CC Chlamydia pneumoniae. The test comprises detecting antibodies specific  
 CC for Omp4-Omp15 or detecting nucleic acid fragments encoding these outer  
 CC membrane proteins, especially by PCR. The proteins are also used in the  
 CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids and  
 CC proteins can also be used in the immunization of mammals, the nucleic

CC acids being particularly useful as DNA vaccines for effecting in vivo  
 CC expression of antigens. The vaccines may also prevent atherosclerosis and  
 CC bronchial asthma, which are possibly associated with C. pneumoniae.  
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 928 AA;

QY Query Match 1.3%; Score 12; DB 2; Length 928;  
 Best Local Similarity 100.0%; Pred. No. 0.068;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 910 ELRGSSRNRYND 921  
 |||||  
 910 ELRGSSRNRYND 921

RESULT 9  
 AAY94327

ID AAY94327 standard; protein; 928 AA.

XX AAY94327;

DT 12-SEP-2003 (revised)

DT 11-AUG-2000 (first entry)

XX Chlamydia pneumoniae 98kD putative outer membrane protein.

KM Chlamydia; antigen; vaccine; infection; outer membrane protein.

XX Chlamydia pneumoniae.

PN WO200026237-A2.

PD 11-MAY-2000.

PF 29-OCT-1999; 99MO-GB003579.

PR 29-OCT-1998; 98US-0106070P.

PR 01-MAR-1999; 99US-0122066P.

PR 27-OCT-1999; 99US-00428122.

PA (CONN-) CONNAUGHT LAB LTD.

PI Mordin AD, Oomen RP, Dunn PL;

DR WPI; 2000-365569/31.

DR N-PSDB; AAA27021.

PT Novel Chlamydia 98 kDa putative outer membrane protein antigen, used for  
 vaccination and protection against Chlamydia infection.

PS Claim 6; Fig 1; 93pp; English.

XX The present sequence is the 98kDa putative outer membrane protein from  
 CC Chlamydia pneumoniae. The genomic sequence was amplified using two PCR  
 CC primers. The 5' primer contains a NotI restriction site, a ribosome  
 CC binding site, an initiation codon and a sequence close to the 5' end of  
 CC the 98kDa putative outer membrane protein coding sequence. The 3' primer  
 CC contains the sequence encoding the C-terminal sequence of the putative  
 CC outer membrane protein and a BglI restriction site. The stop codon was  
 CC excluded and an additional nucleotide was inserted to obtain an in-frame  
 CC C-terminal fusion with the Histidine tag. The PCR product was cloned into  
 CC a eukaryotic expression vector (pCA-Myc-His) by restricting both the  
 CC vector and the PCR product with NotI and BamHI and performing a ligation  
 CC reaction. This expression vector was injected intramuscularly and  
 CC intranasally into mice, which were subsequently inoculated with Chlamydia  
 CC pneumoniae. The chlamydial lung titers of the immunised mice were lower  
 CC than those of the controls. Thus the 98kDa putative outer membrane  
 CC protein can be used as a vaccine to provide protection against Chlamydia  
 CC infections, especially Chlamydia pneumoniae infections. The present  
 CC polypeptide may also be administered orally to treat Chlamydia infection.  
 CC (Updated on 12-SEP-2003 to standardise OS field)

SQ Sequence 928 AA;  
Query Match 1.3%; Score 12; DB 3; Length 928;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 910 ELRGSSRNRYND 921  
910 ELRGSSRNRYND 921  
Db 910 ELRGSSRNRYND 921  
RESULT 10  
ADW30988  
ID ADW30988 standard; peptide; 10 AA.  
AC ADW30988;  
XX  
XX 10-MAR-2005 (first entry)  
DE HLA binding epitope #1738.  
XX  
XX Virucide; cytosstatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
KM viral disease; cancer.  
XX  
XX Unidentified.  
OS  
XX WO2003040165-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 18-OCT-2001; 2001WO-US051650.  
XX  
XX 19-OCT-2000; 2000US-0242350P.  
XX  
XX 20-APR-2001; 2001US-0285624P.  
XX  
XX (EPIM-) EPIMMONE INC.  
XX  
XX Sette A, Sidney J, Southwood S;  
XX  
XX WPI; 2003-441519/41.  
XX  
XX New composition comprising at least one peptide having allele-specific  
PT binding motifs for HLA, useful for preventing, treating or diagnosing  
PT viral diseases and cancer.  
XX  
XX  
XX Claim 1; Page 52-379; 382pp; English.  
XX  
XX The invention relates to a composition comprising at least one peptide  
CC having an isolated, prepared epitope selected from any of the sequences  
CC from 30 lists given in the specification. Also disclosed is a method for  
CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
CC patient expressing a specific MHC class I allele by contacting cytotoxic  
CC T cells from the patient with the composition cited above. The  
CC composition comprises an epitope that is joined by an amino acid linker.  
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
CC binds to a complex of the HLA molecule and the epitope. Specifically  
CC claimed are peptides having allele-specific binding motifs for HLA. The  
CC compositions and methods are useful for preventing, treating or  
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
CC diagnostic agents for evaluating immune responses, for making antibodies  
CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-  
CC ADW37745 represent epitopes of the invention as given in Tables 2-31.  
XX  
XX  
SQ Sequence 10 AA;  
Query Match 1.1%; Score 10; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 528 QLFSLKITY 537

Db 1 QLFSLKITY 10  
RESULT 11  
ADW30926  
ID ADW30926 standard; peptide; 10 AA.  
AC ADW30926;  
XX  
XX 10-MAR-2005 (first entry)  
DE HLA binding epitope #1676.  
XX  
XX Virucide; cytosstatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
KM viral disease; cancer.  
XX  
XX Unidentified.  
OS  
XX WO2003040165-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 18-OCT-2001; 2001WO-US051650.  
XX  
XX 19-OCT-2000; 2000US-0242350P.  
XX  
XX 20-APR-2001; 2001US-0285624P.  
XX  
XX (EPIM-) EPIMMONE INC.  
XX  
XX Sette A, Sidney J, Southwood S;  
XX  
XX WPI; 2003-441519/41.  
XX  
XX New composition comprising at least one peptide having allele-specific  
PT binding motifs for HLA, useful for preventing, treating or diagnosing  
PT viral diseases and cancer.  
XX  
XX  
XX Claim 1; Page 52-379; 382pp; English.  
XX  
XX The invention relates to a composition comprising at least one peptide  
CC having an isolated, prepared epitope selected from any of the sequences  
CC from 30 lists given in the specification. Also disclosed is a method for  
CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
CC patient expressing a specific MHC class I allele by contacting cytotoxic  
CC T cells from the patient with the composition cited above. The  
CC composition comprises an epitope that is joined by an amino acid linker.  
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
CC binds to a complex of the HLA molecule and the epitope. Specifically  
CC claimed are peptides having allele-specific binding motifs for HLA. The  
CC compositions and methods are useful for preventing, treating or  
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
CC diagnostic agents for evaluating immune responses, for making antibodies  
CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-  
CC ADW37745 represent epitopes of the invention as given in Tables 2-31.  
XX  
XX  
SQ Sequence 10 AA;  
Query Match 1.1%; Score 10; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 601 ALVNCNTLMGV 610  
1 ALVNCNTLMGV 10  
Db 1 ALVNCNTLMGV 10  
RESULT 12  
ADW30940  
ID ADW30940 standard; peptide; 10 AA.

XX AC ADW30940;  
 XX 10-MAR-2005 (first entry)  
 XX  
 XX HLA binding: epitope #1690.  
 XX  
 XX Varnicide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
 KM viral disease; cancer.  
 XX  
 XX Unidentified.  
 OS  
 XX WO2003040165-A2.  
 PN  
 XX 15-MAY-2003.  
 PD  
 XX 18-OCT-2001; 2001WO-US051650.  
 PF  
 XX 19-OCT-2000; 2000US-0242350P.  
 PR 20-APR-2001; 2001US-0285624P.  
 XX  
 XX (EPLM-) EPLIMUNE INC.  
 PA  
 XX Sette A, Sidney J, Southwood S;  
 PI  
 XX WPI; 2003-441519/41.  
 DR  
 XX  
 XX New composition comprising at least one peptide having allele-specific  
 PT binding motifs for HLA, useful for preventing, treating or diagnosing  
 PT viral diseases and cancer.  
 XX  
 XX Claim 1; Page 52-379; 382pp; English.  
 PS  
 XX The invention relates to a composition comprising at least one peptide  
 CC having an isolated, prepared epitope selected from any of the sequences  
 CC from 30 lists given in the specification. Also disclosed is a method for  
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
 CC patient expressing a specific MHC class I allele by contacting cytotoxic  
 CC T cells from the patient with the composition cited above. The  
 CC composition comprises an epitope that is joined by an amino acid linker.  
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
 CC binds to a complex of the HLA molecule and the epitope. Specifically  
 CC claimed are peptides having allele-specific binding motifs for HLA. The  
 CC compositions and methods are useful for preventing, treating or  
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
 CC diagnostic agents for evaluating immune responses, for making antibodies  
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-  
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.  
 CC  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 1.1%; Score 10; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 KM Chlamydial infection; antigen; immunogen; vaccine; diagnosis;  
 KM human respiratory disease; cardiovascular disease; atherosclerosis;  
 KM coronary artery disease; carotid artery stenosis; myocardial infarction;  
 KM cerebrovascular disease; aortic aneurysm; claudication; stroke;  
 KM strain CWL029.  
 XX  
 XX Chlamydothila pneumoniae.  
 OS  
 XX WO200202606-A2.  
 PN  
 XX 10-JAN-2002.  
 PD  
 XX  
 XX 03-JUL-2001; 2001WO-1B001445.  
 PF  
 XX 03-JUL-2000; 2000GB-00016363.  
 PR 11-JUL-2000; 2000GB-00017047.  
 PR 21-JUL-2000; 2000GB-00017983.  
 PR 07-AUG-2000; 2000GB-00019368.  
 PR 18-AUG-2000; 2000GB-00020440.  
 PR 14-SEP-2000; 2000GB-00022583.  
 PR 10-NOV-2000; 2000GB-00027549.  
 PR 22-DEC-2000; 2000GB-00031706.  
 XX  
 XX (CHIR-) CHIRON SPA.  
 PA  
 XX  
 XX Ractl G, Grandi G;  
 PI  
 XX WPI; 2002-154726/20.  
 DR N-PSDB; ABL91194.  
 XX  
 XX Novel Chlamydia pneumoniae protein useful in the manufacture of a  
 PT medicament for treatment or prevention of infection due to Chlamydia,  
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.  
 XX  
 XX Claim 1; Page 51; 364pp; English.  
 PS  
 XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia  
 CC pneumoniae (strain CWL029) and ABL91184-ABL91373 represent DNA encoding  
 CC them. The proteins are predicted to be immunogenic and may therefore be  
 CC useful in vaccine production and for diagnostic purposes. Chlamydia  
 CC pneumoniae is a common cause of respiratory disease in humans, and is  
 CC also involved in the development of cardiovascular diseases such as  
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,  
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,  
 CC claudication and stroke. The proteins and nucleic acids of the invention  
 CC may be used in vaccines and pharmaceutical compositions for the  
 CC prevention or treatment of chlamydial infections, particularly Chlamydia  
 CC pneumoniae infections. The proteins may also be used in the detection of  
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched  
 CC DNA probe assay or blotting techniques for determining Chlamydia  
 CC pneumoniae gene expression. The present sequence represents a  
 CC specifically claimed Chlamydia pneumoniae protein of the invention.  
 CC (Updated on 29-AUG-2003 to standardise OS field)  
 CC  
 XX  
 XX Sequence 395 AA;  
 SQ  
 Query Match 1.1%; Score 10; DB 5; Length 395;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 13-SEP-1999 (first entry)  
 XX Chlamydia pneumoniae transmembrane protein sequence.  
 DE  
 XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
 KM neutralising epitope.  
 XX  
 OS Chlamydia pneumoniae.  
 XX  
 PN MO9927105-A2.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PF 20-NOV-1998; 98WO-IB001890.  
 XX  
 PR 21-NOV-1997; 97FR-00014673.  
 PR 04-NOV-1998; 98US-0107078P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Griffais R;  
 XX  
 DR WPI; 1999-357842/30.  
 XX  
 PT Genome sequence of Chlamydia pneumoniae.  
 PS Page 637-638; Disclosure; 1912pp; English.  
 XX  
 CC AAY3484-Y35879 represent the proteins encoded by all the open reading  
 CC frames in the complete genome (see AAY9190) of Chlamydia pneumoniae. C.  
 CC pneumoniae causes respiratory disease such as pneumonia and bronchitis  
 CC and is thought to be a contributing factor in heart disease, sarcoidosis,  
 CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The  
 CC polypeptides encoded by the open reading frames of the C. pneumoniae  
 CC genome (see AAY3484-Y35879) can be used in immunogenic compositions as  
 CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also  
 CC be used as immunogenic compositions, especially where the vector directs  
 CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17  
 CC -OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 450 AA;  
 Query Match 1.1%; Score 10; DB 2; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 910 ELRGSSRNYN 919  
 |||||||||  
 Db 432 ELRGSSRNYN 441  
 RESULT 15  
 ABP56002  
 ID ABP56002 standard; protein; 839 AA.  
 XX  
 AC ABP56002;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Chlamydia psittaci antigen CP4#4 protein SEQ ID NO:23.  
 XX  
 KW Chlamydia psittaci; vaccination; vaccine; antigen; immune response;  
 KM immunisation; antibacterial; infection.  
 XX  
 OS Chlamydia caviae.  
 XX  
 OS MO200253588-A2.  
 PN  
 PD 11-JUL-2002.  
 XX  
 PF 17-DEC-2001; 2001WO-US048715.

XX  
 PR 15-DEC-2000; 2000US-00738269.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 PI Johnston SA, Stenke-Hale K, Sykes KF, Kaltenboeck B;  
 XX  
 DR WPI; 2002-537942/57.  
 DR N-PSDB; ABC04758.  
 XX  
 PT Vaccine for immunization of animal, preferably bovine, against Chlamydia  
 PT psittaci, comprises at least one polynucleotide having a C. psittaci  
 PT sequence, or at least one C. psittaci antigen.  
 PS  
 PS Claim 9; Page 127-129; 164pp; English.  
 XX  
 CC The present invention describes a vaccine (I) for the immunisation of an  
 CC animal against Chlamydia psittaci comprising at least one polynucleotide  
 CC (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen  
 CC (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is  
 CC useful for the immunisation of a bovine. The present sequence represents  
 CC a C. psittaci antigen from the present invention. (Updated on 29-AUG-2003  
 CC to standardise OS field)  
 XX  
 SQ Sequence 839 AA;  
 Query Match 1.1%; Score 10; DB 5; Length 839;  
 Best Local Similarity 100.0%; Pred. No. 5.5;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 79 TDNLTFILGNG 88  
 |||||||||  
 Db 81 TDNLTFILGNG 90  
 Search completed: November 25, 2005, 14:37:12  
 Job time : 116.724 secs



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## OM protein - protein search, using sw model

Run on: November 25, 2005, 14:22:05 ; Search time 24.3603 Seconds  
(without alignments)  
3665.352 Million cell updates/sec

Title: US-09-446-677b-2

Perfect score: 928

Sequence: 1 MKTSIPWVLVSSVLAFSCHL.....MEIRGSSRYNVVDVGTKEKF 928

Scoring table: OLIGO

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID     | Description            |
|------------|-------|-------------|--------|----|--------|------------------------|
| 1          | 928   | 100.0       | 928    | 2  | D72077 | polymorphic outer      |
| 2          | 928   | 100.0       | 928    | 2  | H86546 | polymorphic outer      |
| 3          | 928   | 100.0       | 949    | 2  | F81591 | polymorphic membra     |
| 4          | 12    | 1.3         | 772    | 2  | H86492 | pmp_3 [imported] -     |
| 5          | 10    | 1.1         | 445    | 2  | E86493 | pmp_5 [imported] -     |
| 6          | 9     | 1.0         | 261    | 2  | F82795 | hypothetical prote     |
| 7          | 9     | 1.0         | 737    | 2  | SS5117 | probable membrane      |
| 8          | 9     | 1.0         | 930    | 2  | D86546 | polymorphic outer      |
| 9          | 9     | 1.0         | 930    | 2  | D72078 | polymorphic membra     |
| 10         | 9     | 1.0         | 930    | 2  | A81591 | polymorphic membra     |
| 11         | 8     | 0.9         | 218    | 2  | T01412 | heat shock protein     |
| 12         | 8     | 0.9         | 241    | 2  | H82072 | DNA repair protein     |
| 13         | 8     | 0.9         | 342    | 2  | S75783 | dtmB, glucanase 4.6-de |
| 14         | 8     | 0.9         | 391    | 2  | S06969 | pectate lyase (EC      |
| 15         | 8     | 0.9         | 406    | 1  | UC5041 | fosmidomycin resis     |
| 16         | 8     | 0.9         | 406    | 2  | H85545 | fosmidomycin resis     |
| 17         | 8     | 0.9         | 406    | 2  | D90695 | fosmidomycin resis     |
| 18         | 8     | 0.9         | 427    | 2  | A86493 | carboxyl-terminal      |
| 19         | 8     | 0.9         | 445    | 2  | AD2023 | probable oxidoredu     |
| 20         | 8     | 0.9         | 466    | 2  | B69842 | sulfate adenylylitr    |
| 21         | 8     | 0.9         | 469    | 2  | TS2659 | ecdysteroid-induce     |
| 22         | 8     | 0.9         | 711    | 2  | S43464 | polymorphic membra     |
| 23         | 8     | 0.9         | 922    | 2  | F81539 | polymorphic membra     |
| 24         | 8     | 0.9         | 922    | 2  | B72131 | polymorphic outer      |
| 25         | 8     | 0.9         | 922    | 2  | H86491 | polymorphic outer      |
| 26         | 8     | 0.9         | 928    | 2  | G86546 | polymorphic membra     |
| 27         | 8     | 0.9         | 928    | 2  | G81591 | polymorphic membra     |
| 28         | 8     | 0.9         | 973    | 2  | B86547 | polymorphic outer      |
| 29         | 8     | 0.9         | 973    | 2  | F72076 | polymorphic outer      |

|    |   |     |      |   |        |                    |
|----|---|-----|------|---|--------|--------------------|
| 30 | 8 | 0.9 | 995  | 2 | C81593 | polymorphic membra |
| 31 | 8 | 0.9 | 1013 | 2 | G71460 | probable outer mem |
| 32 | 8 | 0.9 | 1276 | 2 | B86546 | polymorphic outer  |
| 33 | 8 | 0.9 | 1276 | 2 | C81591 | polymorphic membra |
| 34 | 8 | 0.9 | 1407 | 2 | B72078 | polymorphic outer  |
| 35 | 8 | 0.9 | 1723 | 2 | H86557 | polymorphic membra |
| 36 | 8 | 0.9 | 1723 | 2 | E72067 | polymorphic membra |
| 37 | 8 | 0.9 | 1732 | 2 | C81601 | polymorphic membra |
| 38 | 7 | 0.8 | 42   | 2 | I51291 | aldolase C - chick |
| 39 | 7 | 0.8 | 43   | 2 | A35771 | dnak-type molecule |
| 40 | 7 | 0.8 | 56   | 2 | S46471 | IG heavy chain V-r |
| 41 | 7 | 0.8 | 78   | 2 | S46461 | IG heavy chain V-r |
| 42 | 7 | 0.8 | 81   | 2 | B81133 | hypothetical prote |
| 43 | 7 | 0.8 | 91   | 1 | EP82   | phospholipid trans |
| 44 | 7 | 0.8 | 96   | 2 | S26923 | IG heavy chain V r |
| 45 | 7 | 0.8 | 96   | 2 | S26924 | IG heavy chain V r |

## ALIGNMENTS

## RESULT 1

D72077 polymorphic outer membrane protein g family - Chlamydia pneumoniae (strain CWL029)  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: D72077  
R:Kalmun, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; WUID:9920606; PMID:10192388  
A:Accession: D72077  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-928 <ARN>  
A:References: UNIPROT:O86164; UNIPARC:UPI000002FFEF; GB:AE001628; GB:AE001363; NID:  
A:Experimental source: strain CWL029  
C:Genetics:  
A:Gene: pmp\_11  
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

| Query Match | Best Local Similarity | 100.0%; Score 928; DB 2; Length 928;                            |
|-------------|-----------------------|---|
| Matches     | 928; Conservative     | 0; Mismatches 0; Indels 0; Gaps 0;                              |
| QY          | 1                     | MKTSIPWVLVSSVLAFSCHLQSLANEELISPPDSFNGNIDSGTFPPKTSATYSLTGDF 60   |
| DB          | 1                     | MKTSIPWVLVSSVLAFSCHLQSLANEELISPPDSFNGNIDSGTFPPKTSATYSLTGDF 60   |
| QY          | 61                    | FYEPGKGTLPDSQCFQQTNDLTFIENGHSLTFGFIDAGTHAGAAATYANKNLFPSSGS 120  |
| DB          | 61                    | FYEPGKGTLPDSQCFQQTNDLTFIENGHSLTFGFIDAGTHAGAAATYANKNLFPSSGS 120  |
| QY          | 121                   | LISFDSPPSTVTTGGTLLSAGVNLLENIRKLVVAGNFSTADGAIKASFLTGTSGD 180     |
| DB          | 121                   | LISFDSPPSTVTTGGTLLSAGVNLLENIRKLVVAGNFSTADGAIKASFLTGTSGD 180     |
| QY          | 181                   | ALPSSNNSSTKGALATTGARIANNVGVRLSNIASTSGAIDEGSIISNNKFLYF 240       |
| DB          | 181                   | ALPSSNNSSTKGALATTGARIANNVGVRLSNIASTSGAIDEGSIISNNKFLYF 240       |
| QY          | 241                   | EGNAKTGTGALCNTKASGPPELLISNNKTLIFASVNAETSGAIIHAKKLLASGGFTFF 300  |
| DB          | 241                   | EGNAKTGTGALCNTKASGPPELLISNNKTLIFASVNAETSGAIIHAKKLLASGGFTFF 300  |
| QY          | 301                   | LNNVSSATPKGALSIDASGELSLAETGNTTFVRNLTITTTGSDTDPKRNAINIGSNK 360   |
| DB          | 301                   | LNNVSSATPKGALSIDASGELSLAETGNTTFVRNLTITTTGSDTDPKRNAINIGSNK 360   |
| QY          | 361                   | FTELRAAKNHTLFFPDITSEGTSSDVLLKINNGSAGALNPYGGTILFSGETLTADLAKA 420 |
| DB          | 361                   | FTELRAAKNHTLFFPDITSEGTSSDVLLKINNGSAGALNPYGGTILFSGETLTADLAKA 420 |

Qy 421 DNKSSFTQPVSLSGKLLQKGVLTSTSPSOEAGSLGMDSGTLLTAGSITTTNLG 480  
Db 421 DNKSSFTQPVSLSGKLLQKGVLTSTSPSOEAGSLGMDSGTLLTAGSITTTNLG 480  
Qy 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIVESHMFSDQLFSLKITVDAD 540  
Db 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIVESHMFSDQLFSLKITVDAD 540  
Qy 541 VDTNVDLSSLIPVAEDPNSSEYFQOGQNNVMTTDTATNTKEATATWTKGFPVSPERKS 600  
Db 541 VDTNVDLSSLIPVAEDPNSSEYFQOGQNNVMTTDTATNTKEATATWTKGFPVSPERKS 600  
Qy 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWWSMTNPLHKTGDENRKGFRHTSGG 660  
Db 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWWSMTNPLHKTGDENRKGFRHTSGG 660  
Qy 661 YVIGSANTPKODLFTFAFCHLPARDKCFIAHNSRTYGGTLFFKHSHTLQPNYLRIG 720  
Db 661 YVIGSANTPKODLFTFAFCHLPARDKCFIAHNSRTYGGTLFFKHSHTLQPNYLRIG 720  
Qy 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSGMSNECIAIGLDL 780  
Db 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSGMSNECIAIGLDL 780  
Qy 781 PVLNSNHPLEKFTIPQMKVEMVYVSONSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
Db 781 PVLNSNHPLEKFTIPQMKVEMVYVSONSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
Qy 841 IGDSTYDLSGFPVSDVYRRNPQSTATLVMSPDWKIRGSLRQAFLLRGSNNVYNSN 900  
Db 841 IGDSTYDLSGFPVSDVYRRNPQSTATLVMSPDWKIRGSLRQAFLLRGSNNVYNSN 900  
Qy 901 CELFGHYAMELRGSSRRNVNDVGTCLRF 928  
Db 901 CELFGHYAMELRGSSRRNVNDVGTCLRF 928

## RESULT 2

H86546  
polymorphic outer membrane protein G family [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H86546  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: A86491; PMID:20330349; PMID:10871362  
A:Accession: H86546  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-928 <STO>  
A:Cross-references: UNIPROT:O86164; UNIPARC:UPI000002PFEP; GB:BA000008; NID:g8978822; PI  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: pmp\_11  
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 100.0%; Score 928; DB 2; Length 928;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKTSLPWLVSVLAFSCHLQSLANBELSPDPSFNGNIDSGTFPKTSATTVSLTGVF 60  
Db 1 MKTSLPWLVSVLAFSCHLQSLANBELSPDPSFNGNIDSGTFPKTSATTVSLTGVF 60  
Qy 61 FYEPKGPPLSDCKKOTTDNITFLGNGHSLTFGIDAGTAGAASLTANKNLTFSGFS 120  
Db 61 FYEPKGPPLSDCKKOTTDNITFLGNGHSLTFGIDAGTAGAASLTANKNLTFSGFS 120  
Qy 121 LLSFSSSTTYTTCOGTLLSSAGVNLNIRKLVVAGNPSRADGAIIGASFLTLGTSGD 180  
Db 121 LLSFSSSTTYTTCOGTLLSSAGVNLNIRKLVVAGNPSRADGAIIGASFLTLGTSGD 180

Qy 181 ALFSSNNSSTKGAIAITTAGARIANNNTGYVRLSNIASTSGAIDDEGTSILSNKFLYF 240  
Db 181 ALFSSNNSSTKGAIAITTAGARIANNNTGYVRLSNIASTSGAIDDEGTSILSNKFLYF 240  
Qy 241 EGNAAATTGALCNTAQSAPPELLISNNKTLFASVVAATSGAIAHAKKALASSGFTFF 300  
Db 241 EGNAAATTGALCNTAQSAPPELLISNNKTLFASVVAATSGAIAHAKKALASSGFTFF 300  
Qy 301 LRNNSSATPKGAIISIDASGELSIAETGNITFVANTLTTTGSTDTPPKRNAINISNGK 360  
Db 301 LRNNSSATPKGAIISIDASGELSIAETGNITFVANTLTTTGSTDTPPKRNAINISNGK 360  
Qy 361 FTELRAAKNHTTFPYDPTSEGTSDVLKINNSAGALNPYOGTILFSGETLTADLKYA 420  
Db 361 FTELRAAKNHTTFPYDPTSEGTSDVLKINNSAGALNPYOGTILFSGETLTADLKYA 420  
Qy 421 DNKSSFTQPVSLSGKLLQKGVLTSTSPSOEAGSLGMDSGTLLTAGSITTTNLG 480  
Db 421 DNKSSFTQPVSLSGKLLQKGVLTSTSPSOEAGSLGMDSGTLLTAGSITTTNLG 480  
Qy 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIVESHMFSDQLFSLKITVDAD 540  
Db 481 INVDSLGLKQPVSLTAKGASNKVIVSGKLNLDIEGNIVESHMFSDQLFSLKITVDAD 540  
Qy 541 VDTNVDLSSLIPVAEDPNSSEYFQOGQNNVMTTDTATNTKEATATWTKGFPVSPERKS 600  
Db 541 VDTNVDLSSLIPVAEDPNSSEYFQOGQNNVMTTDTATNTKEATATWTKGFPVSPERKS 600  
Qy 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWWSMTNPLHKTGDENRKGFRHTSGG 660  
Db 601 ALVCNTLMGVFTDIRSLQQLVEIGATGMEHKQFWWSMTNPLHKTGDENRKGFRHTSGG 660  
Qy 661 YVIGSANTPKODLFTFAFCHLPARDKCFIAHNSRTYGGTLFFKHSHTLQPNYLRIG 720  
Db 661 YVIGSANTPKODLFTFAFCHLPARDKCFIAHNSRTYGGTLFFKHSHTLQPNYLRIG 720  
Qy 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSGMSNECIAIGLDL 780  
Db 721 RAKFSESAIEKFPREIPLALDVQVSFSDNRMETHTYSLPESGSGMSNECIAIGLDL 780  
Qy 781 PVLNSNHPLEKFTIPQMKVEMVYVSONSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
Db 781 PVLNSNHPLEKFTIPQMKVEMVYVSONSPFESSSDGRGFSIGRLNLISIPVGAKEVQGD 840  
Qy 841 IGDSTYDLSGFPVSDVYRRNPQSTATLVMSPDWKIRGSLRQAFLLRGSNNVYNSN 900  
Db 841 IGDSTYDLSGFPVSDVYRRNPQSTATLVMSPDWKIRGSLRQAFLLRGSNNVYNSN 900  
Qy 901 CELFGHYAMELRGSSRRNVNDVGTCLRF 928  
Db 901 CELFGHYAMELRGSSRRNVNDVGTCLRF 928

## RESULT 3

F81591  
polymorphic membrane protein G family CP0302 [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 15-Jun-2001  
C:Accession: F81591  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heldelberg, J.F.; White, O.; Hickey, J.  
, C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis Mdn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; PMID:20150255; PMID:10684935  
A:Accession: F81591  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-949 <REA>  
A:Cross-references: UNIPARC:UPI00001655FA; GB:AE002192; GB:AE002161; NID:g7189226; PIDN:  
A:Experimental source: strain AR39, HU cells  
C:Genetics:  
A:Gene: CP0302  
C:Superfamily: Chlamydia pneumoniae polymorphic outer membrane protein G

Query Match 100.0%; Score 928; DB 2; Length 949;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTSTWVSVSVLAFSCHLQSLANBELLSDDDFNCGNIDSGTFPTKTSATTVSLTGDFV 60  
 DB 22 MKTSTWVSVSVLAFSCHLQSLANBELLSDDDFNCGNIDSGTFPTKTSATTVSLTGDFV 81  
 QY 61 FYRPGKGTPLSDSCFQOTDNLTFPLNGHSLTRGPTLDAGHAGAATASTANKLTSGGS 120  
 DB 82 FYRPGKGTPLSDSCFQOTDNLTFPLNGHSLTRGPTLDAGHAGAATASTANKLTSGGS 141  
 QY 121 LLSFDSSTPTVTTGGCTLSSAGGVNLENIRKLVAGNFSTADGAIKGAFLITGSGD 180  
 DB 142 LLSFDSSTPTVTTGGCTLSSAGGVNLENIRKLVAGNFSTADGAIKGAFLITGSGD 201  
 QY 181 ALFSNNSSSTKGAIAATTAGARIANNTRYVPLSNIASTSGAIDDEGSIISNNKFLYF 240  
 DB 202 ALFSNNSSSTKGAIAATTAGARIANNTRYVPLSNIASTSGAIDDEGSIISNNKFLYF 261  
 QY 241 EGNAAATTTGAIICNTAKASGPELIIISNNKTLIFASNAVAETSGAIIAKKALSSGGTFE 300  
 DB 262 EGNAAATTTGAIICNTAKASGPELIIISNNKTLIFASNAVAETSGAIIAKKALSSGGTFE 321  
 QY 301 LRNNSSATPKGGAISIDAGSELISAETGNITFVRNTLTSTSTDPKNAINIGSNGK 360  
 DB 322 LRNNSSATPKGGAISIDAGSELISAETGNITFVRNTLTSTSTDPKNAINIGSNGK 381  
 QY 361 FTFLRAAKNHTIFFYDPTSEGTSDVLKINNSAGALNPDYQCTILFSGETTLADELKA 420  
 DB 382 FTFLRAAKNHTIFFYDPTSEGTSDVLKINNSAGALNPDYQCTILFSGETTLADELKA 441  
 QY 421 DNKSSFTQVSLSGGTLLOKVTLESTSFSGEAGSLCMBDGTTLSTAGSTTTTNIG 480  
 DB 442 DNKSSFTQVSLSGGTLLOKVTLESTSFSGEAGSLCMBDGTTLSTAGSTTTTNIG 501  
 QY 481 INVDISGLKQVSLTAKGANKYIVSGKLNLDIEGIVESHMFSDQLFSLKITVDAD 540  
 DB 502 INVDISGLKQVSLTAKGANKYIVSGKLNLDIEGIVESHMFSDQLFSLKITVDAD 561  
 QY 541 VDTNVDISLIPVPAEDPNSEYGFQGMVNMWTTDTANTKEATATWTKTGVPSPERKS 600  
 DB 562 VDTNVDISLIPVPAEDPNSEYGFQGMVNMWTTDTANTKEATATWTKTGVPSPERKS 621  
 QY 601 ALVCNTLMGVTFTIRSLQQLVEIGATGMEHKGFVWSMTNPLHKTGDENRKGFRTSGG 660  
 DB 622 ALVCNTLMGVTFTIRSLQQLVEIGATGMEHKGFVWSMTNPLHKTGDENRKGFRTSGG 681  
 QY 661 YVIFGSAHPTKDLTFPACHLFPARDKCFIAHNNSTYGTLPFKHSHTLQPNYLRIG 720  
 DB 682 YVIFGSAHPTKDLTFPACHLFPARDKCFIAHNNSTYGTLPFKHSHTLQPNYLRIG 741  
 QY 721 RAFFESALIEKFPREIPLALDVQVSFSDNRMETHYTSLPESGGSWNECIAGIGLDL 780  
 DB 742 RAFFESALIEKFPREIPLALDVQVSFSDNRMETHYTSLPESGGSWNECIAGIGLDL 801  
 QY 781 PFLVLSNHPILFKTFIPOMKVEMYVVSNSFPESSDRGSGISGLMLSLIPVGAKEYQGD 840  
 DB 802 PFLVLSNHPILFKTFIPOMKVEMYVVSNSFPESSDRGSGISGLMLSLIPVGAKEYQGD 861  
 QY 841 IGSYTYTDLGFFVSDVYRRNNPOSTATLWMSPDMSKIRGNLSROAFILGNNYVNSN 900  
 DB 862 IGSYTYTDLGFFVSDVYRRNNPOSTATLWMSPDMSKIRGNLSROAFILGNNYVNSN 921  
 QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928  
 DB 922 CELFGHYAMELRGSSRNRYNDVGTCLRF 949

RESULT 4  
 H86492  
 Pmp\_3 [imported] - Chlamydia pneumoniae (strain J138)

C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C/Accession: H86492  
 R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi  
 Nucleic Acids Res. 28, 2311-2314, 2000  
 A/Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
 A/Reference number: A86491; MUID:20330349; PMID:10871362  
 A/Accession: H86492  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-772 <STO>  
 A/Cross-references: UNIPROT:Q9RB71; UNIPARC:UPI00000CCC33; GB:BA000008; NID:98978389; PII  
 A/Experimental source: strain J138  
 C/Genetics:  
 A/Gene: pmp\_3\_2

Query Match 1.3%; Score 12; DB 2; Length 772;  
 Best Local Similarity 100.0%; Pred. No. 0.0044;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYND 921  
 DB 754 ELRGSSRNRYND 765

RESULT 5  
 H86493  
 Pmp\_5 [imported] - Chlamydia pneumoniae (strain J138)  
 C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C/Accession: H86493  
 R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishi  
 Nucleic Acids Res. 28, 2311-2314, 2000  
 A/Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.  
 A/Reference number: A86491; MUID:20330349; PMID:10871362  
 A/Accession: H86493  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-445 <STO>  
 A/Cross-references: UNIPROT:Q9RB67; UNIPARC:UPI00000CCC32; GB:BA000008; NID:98978394; PII  
 A/Experimental source: strain J138  
 C/Genetics:  
 A/Gene: pmp\_5\_2

Query Match 1.1%; Score 10; DB 2; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYN 919  
 DB 427 ELRGSSRNRYN 436

RESULT 6  
 F82795  
 hypothetical protein XF0515 [imported] - Xylella fastidiosa (strain 945c)  
 C/Species: Xylella fastidiosa  
 C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C/Accession: F82795  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc  
 Nature 406, 151-157, 2000  
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A/Reference number: A82515; MUID:20365717; PMID:10910347  
 A/Note: for a complete list of authors see reference number A53328 below  
 A/Accession: F82795  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-261 <SIM>  
 A/Cross-references: UNIPROT:Q9PF21; UNIPARC:UPI00000C2434; GB:AE003900; GB:AE003849; NID:  
 A/Experimental source: strain 945c  
 R/Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al  
 Birones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canazaro, U.E.A.; Carraro, D.M.; Carreir, H.  
 as-Neto, E.; Docena, C.; El-Dorcy, H.; Facincani, A.P.; Ferreira, A.U.S.

```
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fromm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuname, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tashiro, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0515

Query Match          1.0%; Score 9; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          532 LKKTVDAD 540
          |||||
          4 LKKTVDAD 12

RESULT 7
S55117
probable membrane protein YML002w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YW8270.01; hypothetical protein YW9571.17
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C:Accession: S55117; S53028
R:Gentiles, S.; Bowman, S.
submitted to the EMBL Data Library, June 1995
A:Reference number: S55102
A:Accession: S55117
A:Molecule type: DNA
A:Residues: 1-254 <GEN>
A:Cross-references: UNIPROT:004263; UNIPARC:UPI0000168AB0; EMBL:Z49810; NID:g854472; PID
A:Experimental source: strain AB972
R:Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53028
A:Accession: S53028
A:Molecule type: DNA
A:Residues: 250-737 <DEV>
A:Cross-references: UNIPARC:UPI0000168A84; EMBL:Z48613; NID:g728645; PID:g728646; MIPS:X
A:Experimental source: strain AB972
C:Genetics:
A:Map position: 13L
C:Superfamily: Saccharomyces probable membrane protein YML002w
C:Keywords: transmembrane protein
F:15-31/Domain: transmembrane #status predicted <TM>

Query Match          1.0%; Score 9; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          183 FSNSSSTK 191
          |||||
          48 FSNSSSTK 56

RESULT 8
D86546
polymorphic outer membrane protein G family [imported] - Chlamydomonas reinhardtii (strai
C:Species: Chlamydomonas reinhardtii, Chlamydomonas reinhardtii
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C:Accession: D86546
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydomonas reinhardtii J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: D86546
A:Status: preliminary
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A:Molecule type: DNA
A:Residues: 1-930 <STO>
A:Cross-references: UNIPARC:UPI00001655FB; GB:BA000008; NID:g8978618; PIDN:BA098654.1; G
A:Experimental source: strain J138
C:Genetics:
A:Gene: pmp_8
C:Superfamily: Chlamydomonas reinhardtii polymorphic outer membrane protein G

Query Match          1.0%; Score 9; DB 2; Length 930;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          102 AGAASSTTA 110
          |||||
          107 AGAASSTTA 115

RESULT 9
D72078
polymorphic outer membrane protein g family - Chlamydomonas reinhardtii (strain CML029)
C:Species: Chlamydomonas reinhardtii, Chlamydomonas reinhardtii
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: D72078
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydomonas reinhardtii and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: D72078
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-930 <ARN>
A:Cross-references: UNIPROT:Q9Z393; UNIPARC:UPI000004708C; GB:AE001627; GB:AE001363; NID:
A:Experimental source: strain CML029
C:Genetics:
A:Gene: pmp_8
C:Superfamily: Chlamydomonas reinhardtii polymorphic outer membrane protein G

Query Match          1.0%; Score 9; DB 2; Length 930;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          102 AGAASSTTA 110
          |||||
          107 AGAASSTTA 115

RESULT 10
A81591
polymorphic outer membrane protein G family CP0307 [imported] - Chlamydomonas reinhardtii (strai
C:Species: Chlamydomonas reinhardtii, Chlamydomonas reinhardtii
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81591
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydomonas reinhardtii MoDa and Chlamydomonas reinhardtii AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: A81591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-930 <REA>
A:Cross-references: UNIPROT:Q9Z393; UNIPARC:UPI00001655FB; GB:AE002193; GB:AE002161; NID
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0307
C:Superfamily: Chlamydomonas reinhardtii polymorphic outer membrane protein G

Query Match          1.0%; Score 9; DB 2; Length 930;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          102 AGAASSTTA 110
          |||||
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Db 107 AGAASTTA 115

## RESULT 11

heat shock protein hsp22 precursor, mitochondrial - maize  
C/Species: Zea mays (maize)

C/Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004

C/Accession: T01412

R/Lund, A.A.; Blum, P.H.; Bhattacharjee, D.; Elchou, T.E.

Plant Physiol. 116, 1097-1110, 1998

A/Title: Heat-stress response of maize mitochondria.

A/Reference number: Z14320; MUID:98169424; PMID:9501143

A/Accession: T01412

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-218 &lt;LUN&gt;

A/Cross-references: UNIPROT:O64960; UNIPARC:UPI00000A372C; EMBL:AF035460; NID:g3015620;

A/Experimental source: strain B73

C/Genetics:

A/Genome: hsp22

C/Superfamily: alpha-crystallin-related small heat shock protein

C/Keywords: heat shock; mitochondrion; stress-induced protein

F:1-45/Domain: transit peptide (mitochondrion) #status predicted &lt;TNP&gt;

F:46-218/Product: low molecular weight heat shock protein hsp22 #status predicted &lt;MAT&gt;

Query Match 0.9%; Score 8; DB 2; Length 218;  
Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 SIGRLNLT 828

Db 95 SIGRLNLT 102

## RESULT 12

DNA repair protein Reco VC2459 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
H82072

C/Species: Vibrio cholerae

C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004

C/Accession: H82072

R/Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.U.;

Charadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bae, S.; Qin, H.; Dragol, I.; Sellers, F.

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A/Reference number: A82035; MUID:20406833; PMID:10952301

A/Accession: H82072

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-241 &lt;HEI&gt;

A/Cross-references: UNIPROT:Q9KPB4; UNIPARC:UPI00001335B1; GB:AE004316; GB:AE003852; NID

A/Experimental source: serogroup O1; strain N16961; biotype El Tor

C/Genetics:

A/Genes: VC2459

A/Map position: 1

C/Superfamily: reco protein

Query Match 0.9%; Score 8; DB 2; Length 241;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 DNLTFIGN 87

Db 179 DNLTFIGN 186

## RESULT 13

dtmDglucose 4,6-dehydratase (EC 4.2.1.46) - Synechocystis sp. (strain PCC 6803)  
S75783

C/Species: Synechocystis sp.

A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C/Accession: S75783

R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S.

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S75783

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-342 &lt;KAN&gt;

A/Cross-references: UNIPROT:Q55420; UNIPARC:UPI00000D3539; EMBL:D64003; GB:AB001339; NID:

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C/Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology

C/Keywords: carbon-oxygen lyase; hydro-lyase

F:6-33/Domain: UDPglucose 4-epimerase homology &lt;UDP&gt;

Query Match 0.9%; Score 8; DB 2; Length 342;  
Best Local Similarity 100.0%; Pred. No. 23;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 836 FVQGDIGD 843

Db 58 FVQGDIGD 65

## RESULT 14

pectate lyase (EC 4.2.2.2) D precursor - Erwinia chrysanthemi  
S06969

C/Species: Erwinia chrysanthemi

C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004

C/Accession: S06969

R/van Gijsegem, F.

Mol. Microbiol. 3, 1415-1424, 1989

A/Title: Relationship between the pel genes of the pelADE cluster in Erwinia chrysanthemi

A/Reference number: S06968; MUID:90136069; PMID:2615652

A/Accession: S06969

A/Molecule type: DNA

A/Residues: 1-391 &lt;GIJ&gt;

A/Cross-references: UNIPROT:P18209; UNIPARC:UPI000011580; EMBL:X17284; NID:g42343; PIDN:

A/Experimental source: strain B374

C/Genetics:

A/Genes: pelD

C/Superfamily: pectate lyase

C/Keywords: carbon-oxygen lyase

F:1-31/Domain: signal sequence #status predicted &lt;SIG&gt;

F:32-391/Product: pectate lyase D #status predicted &lt;MAT&gt;

Query Match 0.9%; Score 8; DB 2; Length 391;  
Best Local Similarity 100.0%; Pred. No. 26;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 IGSNGKFT 362

Db 123 IGSNGKFT 130

## RESULT 15

foamdomycin resistance protein - Escherichia coli (strain K-12)  
JCS041

C/Species: Escherichia coli

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: JCS041; F64778

R/Fujisaki, S.; Ohnuma, S.; Horiuchi, T.; Takahashi, I.; Teukui, S.; Nishimura, Y.; Nishi

Gene 175, 83-87, 1996

A/Title: Cloning of a gene from Escherichia coli that confers resistance to foamdomycin

A/Reference number: JCS041; MUID:97074653; PMID:8917080

A/Accession: JCS041

A/Molecule type: DNA

A/Residues: 1-406 &lt;FUJ&gt;

A/Cross-references: UNIPROT:P52067; UNIPARC:UPI000012AC73; DDBJ:D73370; NID:g1019359; PII

A/Experimental source: strain DH5alpha

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd  
 .A.; Rose, D.U.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of Escherichia coli K-12.  
 A;Reference number: A64720; MUID:97426617; PMID:9278503  
 A;Accession: F64778  
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-406 <BLAT>  
 A;Cross-references: UNIPARC:UPI000012AC73; GB:AE000154; GB:U00096; NID:G1786683; PIDN:AF  
 A;Experimental source: strain K-12, substrain MG1655  
 C;Genetics:  
 A;Gene: fsr  
 C;Function:  
 A;Description: confers resistance to fosmidomycin  
 C;Superfamily: fosmidomycin resistance protein  
 C;Keywords: antibiotic resistance; transmembrane protein  
 F;104-120/Domain: transmembrane #status predicted <TM1>  
 F;181-197/Domain: transmembrane #status predicted <TM2>  
 F;225-241/Domain: transmembrane #status predicted <TM3>  
 F;267-283/Domain: transmembrane #status predicted <TM4>  
 F;294-310/Domain: transmembrane #status predicted <TM5>  
 F;320-336/Domain: transmembrane #status predicted <TM6>  
 F;358-374/Domain: transmembrane #status predicted <TM7>  
 F;381-397/Domain: transmembrane #status predicted <TM8>

Query Match 0.9% Score 8; DB 1; Length 406;  
 Best local similarity 100.0%; Pred. No. 27;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 102 AGAASSTT 109  
 |||||  
 Db 11 AGAASSTT 18

Search completed: November 25, 2005, 14:48:09  
 Job time : 31.3603 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2005, 14:21:48 ; Search time 141.29 Seconds  
(without alignments)  
4633.951 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 928  
Sequence: 1 MKTSLPWLVSVAFLAFSCHL.....MEIRGSSRNRYVDVGTKLRF 928

Scoring table: OLIGO  
Gapop 60.0 , Gapect 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description  |
|------------|-------|-------------|--------|-------|--------------|
| 1          | 928   | 100.0       | 928    | 1     | PMP11_CHLPN  |
| 2          | 14    | 1.5         | 1024   | 2     | 051637_CHLAB |
| 3          | 12    | 1.3         | 649    | 2     | P71134_CHLAB |
| 4          | 12    | 1.3         | 772    | 2     | 09R871_CHLBN |
| 5          | 12    | 1.3         | 1378   | 2     | 051632_CHLAB |
| 6          | 10    | 1.1         | 252    | 2     | 08V1H7_CHLPS |
| 7          | 10    | 1.1         | 445    | 2     | 07VQ99_CHLBN |
| 8          | 10    | 1.1         | 445    | 2     | 09RB67_CHLBN |
| 9          | 10    | 1.1         | 839    | 2     | P77922_CHLAB |
| 10         | 9     | 1.0         | 261    | 2     | 09PR21_XYLFA |
| 11         | 9     | 1.0         | 337    | 2     | 07NH75_GLOVT |
| 12         | 9     | 1.0         | 475    | 2     | 06W3N9_9PROT |
| 13         | 9     | 1.0         | 737    | 1     | YMA2_YEAST   |
| 14         | 9     | 1.0         | 737    | 2     | 06B2L5_YEAST |
| 15         | 9     | 1.0         | 868    | 2     | 0823X4_CHLCV |
| 16         | 9     | 1.0         | 930    | 1     | PMP8_CHLBN   |
| 17         | 8     | 0.9         | 47     | 2     | 087267_SIVCZ |
| 18         | 8     | 0.9         | 51     | 2     | 087187_SIVCZ |
| 19         | 8     | 0.9         | 51     | 2     | 087191_SIVCZ |
| 20         | 8     | 0.9         | 51     | 2     | 087203_SIVCZ |
| 21         | 8     | 0.9         | 51     | 2     | 087213_SIVCZ |
| 22         | 8     | 0.9         | 51     | 2     | 087263_SIVCZ |
| 23         | 8     | 0.9         | 51     | 2     | 087270_SIVCZ |
| 24         | 8     | 0.9         | 56     | 2     | 04S2C4_TETNG |
| 25         | 8     | 0.9         | 93     | 2     | 07PX31_AMOGA |
| 26         | 8     | 0.9         | 112    | 2     | 076812_AMOGA |
| 27         | 8     | 0.9         | 132    | 2     | 061516_AMOGA |
| 28         | 8     | 0.9         | 123    | 2     | 06Q1B7_PLOIN |
| 29         | 8     | 0.9         | 139    | 2     | 07YR19_PIG   |
| 30         | 8     | 0.9         | 139    | 2     | 07YR11_PIG   |
| 31         | 8     | 0.9         | 143    | 2     | P79123_BOVIN |

|    |   |     |     |   |              |                     |
|----|---|-----|-----|---|--------------|---------------------|
| 32 | 8 | 0.9 | 165 | 2 | Q8D7T9_VIBVU | Q8D7T9_vibrio vuln  |
| 33 | 8 | 0.9 | 168 | 2 | Q6MFA6_PARUM | Q6MFA6_parachlamyd  |
| 34 | 8 | 0.9 | 174 | 2 | Q88Y02_LACPL | Q88Y02_lactobacill  |
| 35 | 8 | 0.9 | 182 | 2 | Q841V9_CAMFE | Q841V9_campylobact  |
| 36 | 8 | 0.9 | 209 | 2 | Q8ENP4_OCEIH | Q8ENP4_oceanobacti  |
| 37 | 8 | 0.9 | 212 | 2 | Q7MEV3_VIBVY | Q7MEV3_vibrio vuln  |
| 38 | 8 | 0.9 | 215 | 2 | Q4UGL2_THEAN | Q4UGL2_thelateria a |
| 39 | 8 | 0.9 | 218 | 2 | Q64960_MAIZE | Q64960_zea mays (m  |
| 40 | 8 | 0.9 | 227 | 2 | Q7S772_NEUCR | Q7S772_neutrospora  |
| 41 | 8 | 0.9 | 241 | 1 | RECO_VIBCH   | Q9KPB4_vibrio chol  |
| 42 | 8 | 0.9 | 243 | 1 | RECO_VIBPA   | Q87JPI_vibrio para  |
| 43 | 8 | 0.9 | 243 | 1 | RECO_VIBVU   | Q8DC74_vibrio vuln  |
| 44 | 8 | 0.9 | 243 | 1 | RECO_VIBVY   | Q7MMP0_vibrio vuln  |
| 45 | 8 | 0.9 | 282 | 2 | Q61LT7_DROME | Q61LT7_drosophila   |

ALIGNMENTS

| ID | EMPI1_CHLPN   | STANDARD:                         | PRT: | 928 AA. |
|----|---|-----------------------------------|------|---------|
| AC | 086164  | Q9K299                            |      |         |
| DT | 16-OCT-2001   | (Rel. 40, Created)                |      |         |
| DT | 16-OCT-2001   | (Rel. 40, Last sequence update)   |      |         |
| DT | 10-MAY-2005   | (Rel. 47, Last annotation update) |      |         |
| DE | Probable outer membrane protein emp1 precursor (Polymorphic membrane protein 11) (outer membrane protein 4) |                                   |      |         |
| GN | Name=emp1; Synonyms=omp4; OrderedLocustName=Cp00449, CP0302, CpB0468;                                       |                                   |      |         |
| OS | Chlamydia pneumoniae (Chlamydia pneumoniae)   |                                   |      |         |
| OC | Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia  |                                   |      |         |
| OX | NCBI_TaxID=83558;   |                                   |      |         |
| RN | [1]   |                                   |      |         |
| RP | NUCLEOTIDE SEQUENCE.  |                                   |      |         |
| RC | STRAIN=CML029/VR-1310;  |                                   |      |         |
| RX | MEDLINE=99081766; PubMed=9864239;   |                                   |      |         |
| RA | Knudsen K., Madsen A.S., Mygind P., Christiansen G., Birkelund S.;  |                                   |      |         |
| RT | Identification of two novel genes encoding 97- to 99-kilodalton outer                                       |                                   |      |         |
| RT | membrane proteins of Chlamydia pneumoniae."   |                                   |      |         |
| RL | Infect. Immun. 67:375-383 (1999).   |                                   |      |         |
| RN | [2]   |                                   |      |         |
| RP | NUCLEOTIDE SEQUENCE.  |                                   |      |         |
| RC | STRAIN=CML029 / VR1310;   |                                   |      |         |
| RX | MEDLINE=20007584; PubMed=10539856;  |                                   |      |         |
| RA | Christiansen G., Boesen T., Hjerno K., Dagaard L., Mygind P.,   |                                   |      |         |
| RT | Madsen A.S., Knudsen K., Falk E., Birkelund S.;   |                                   |      |         |
| RT | Molecular biology of Chlamydia pneumoniae surface proteins and their  |                                   |      |         |
| RL | role in immunopathogenicity."   |                                   |      |         |
| RL | Am. Heart J. 138:S491-S495(1999).   |                                   |      |         |
| RN | [3]   |                                   |      |         |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  |                                   |      |         |
| RC | STRAIN=CML029.  |                                   |      |         |
| RX | MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716;  |                                   |      |         |
| RA | Kahn S., Mitchell W.P., Marathe R., Lamell C.J., Fan J., Hyman R.W.,  |                                   |      |         |
| RT | Olinger L., Grimwood J., Davis R.W., Stephens R.S.;   |                                   |      |         |
| RT | Comparative genomes of Chlamydia pneumoniae and C. trachomatis."  |                                   |      |         |
| RL | Nat. Genet. 21:385-389(1999).   |                                   |      |         |
| RN | [4]   |                                   |      |         |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  |                                   |      |         |
| RC | STRAIN=AR39;  |                                   |      |         |
| RX | MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;   |                                   |      |         |
| RA | Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,   |                                   |      |         |
| RT | White O., Hickey E.K., Peterson J.D., Ueteyack T.R., Berry K.J.,  |                                   |      |         |
| RA | Baas S., Linher K.D., Wetman J.F., Khouri H.M., Craven B., Bowman C.,                                       |                                   |      |         |
| RA | Dodson R.J., Gwin M.L., Nelson W.C., Deboy R.T., Kolonay J.F.,  |                                   |      |         |
| RT | McClary G., Salzberg S.L., Eisen J.A., Frazer C.M.;   |                                   |      |         |
| RT | Genome sequences of Chlamydia trachomatis Mopn and Chlamydia  |                                   |      |         |
| RL | pneumoniae AR39."   |                                   |      |         |
| RL | Nucleic Acids Res. 28:1397-1406 (2000).   |                                   |      |         |
| RN | [5]   |                                   |      |         |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  |                                   |      |         |
| RC | STRAIN=U138;  |                                   |      |         |
| RX | MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;  |                                   |      |         |

| Query Match | Best Local Similarity | 100.0%     | Score 928 | DB 1   | Length 928 | Matches 928 | Conservative | 0      | Mismatches | 0    | Indels | 0  | Gaps | 0     |
|-------------|-----------------------|------------|-----------|--------|------------|-------------|--------------|--------|------------|------|--------|----|------|-------|
| 1           | MKTSIPWLVSSVLA        | FSCHLOSIAE | ELLSPD    | SPFNGN | IDSQTF     | PPKTSATYS   | LTGVF        | 60     |            |      |        |    |      |       |
| 1           | MKTSIPWLVSSVLA        | FSCHLOSIAE | ELLSPD    | SPFNGN | IDSQTF     | PPKTSATYS   | LTGVF        | 60     |            |      |        |    |      |       |
| 61          | FYEPEKGP              | PLSDSC     | CKQTTD    | NLTFL  | GNHSLTF    | GFIDAG      | THAGAA       | STTANK | LTFS       | SGFS | 120    |    |      |       |
| 61          | FYEPEKGP              | PLSDSC     | CKQTTD    | NLTFL  | GNHSLTF    | GFIDAG      | THAGAA       | STTANK | LTFS       | SGFS | 120    |    |      |       |
| 61          | FYEPEKGP              | PLSDSC     | CKQTTD    | NLTFL  | GNHSLTF    | GFIDAG      | THAGAA       | STTANK | LTFS       | SGFS | 120    |    |      |       |
| 61          | FYEPEKGP              | PLSDSC     | CKQTTD    | NLTFL  | GNHSLTF    | GFIDAG      | THAGAA       | STTANK | LTFS       | SGFS | 120    |    |      |       |
| 61          | FYEPEKGP              | PLSDSC     | CKQTTD    | NLTFL  | GNHSLTF    | GFIDAG      | THAGAA       | STTANK | LTFS       | SGFS | 120    |    |      |       |
| 121         | LISFSSSPT             | TYTTOG     | GLTSSA    | GVNLE  | IRKLV      | VAGNF       | STADG        | GAIKG  | ASFL       | LTG  | TS     | GD | 180  |       |
| 121         | LISFSSSPT             | TYTTOG     | GLTSSA    | GVNLE  | IRKLV      | VAGNF       | STADG        | GAIKG  | ASFL       | LTG  | TS     | GD | 180  |       |
| 121         | LISFSSSPT             | TYTTOG     | GLTSSA    | GVNLE  | IRKLV      | VAGNF       | STADG        | GAIKG  | ASFL       | LTG  | TS     | GD | 180  |       |
| 121         | LISFSSSPT             | TYTTOG     | GLTSSA    | GVNLE  | IRKLV      | VAGNF       | STADG        | GAIKG  | ASFL       | LTG  | TS     | GD | 180  |       |
| 121         | LISFSSSPT             | TYTTOG     | GLTSSA    | GVNLE  | IRKLV      | VAGNF       | STADG        | GAIKG  | ASFL       | LTG  | TS     | GD | 180  |       |
| 181         | ALFSNNS               | STKCGA     | IATTA     | GAIR   | IANTT      | GVRF        | ELSN         | IA     | TS         | SGA  | ID     | DE | GS   | ILSNK |
| 181         | ALFSNNS               | STKCGA     | IATTA     | GAIR   | IANTT      | GVRF        | ELSN         | IA     | TS         | SGA  | ID     | DE | GS   | ILSNK |
| 181         | ALFSNNS               | STKCGA     | IATTA     | GAIR   | IANTT      | GVRF        | ELSN         | IA     | TS         | SGA  | ID     | DE | GS   | ILSNK |
| 181         | ALFSNNS               | STKCGA     | IATTA     | GAIR   | IANTT      | GVRF        | ELSN         | IA     | TS         | SGA  | ID     | DE | GS   | ILSNK |
| 181         | ALFSNNS               | STKCGA     | IATTA     | GAIR   | IANTT      | GVRF        | ELSN         | IA     | TS         | SGA  | ID     | DE | GS   | ILSNK |
| 241         | EGNAK                 | TTGGA      | CNTK      | ASG    | PELL       | ISNN        | KTLIP        | ASN    | V          | A    | ET     | S  | G    | AIHAK |
| 241         | EGNAK                 | TTGGA      | CNTK      | ASG    | PELL       | ISNN        | KTLIP        | ASN    | V          | A    | ET     | S  | G    | AIHAK |
| 241         | EGNAK                 | TTGGA      | CNTK      | ASG    | PELL       | ISNN        | KTLIP        | ASN    | V          | A    | ET     | S  | G    | AIHAK |
| 241         | EGNAK                 | TTGGA      | CNTK      | ASG    | PELL       | ISNN        | KTLIP        | ASN    | V          | A    | ET     | S  | G    | AIHAK |
| 241         | EGNAK                 | TTGGA      | CNTK      | ASG    | PELL       | ISNN        | KTLIP        | ASN    | V          | A    | ET     | S  | G    | AIHAK |
| 301         | LNNV                  | SATPK      | CGA       | IS     | DA         | SG          | EL           | S      | A          | E    | GN     | T  | T    | P     |
| 301         | LNNV                  | SATPK      | CGA       | IS     | DA         | SG          | EL           | S      | A          | E    | GN     | T  | T    | P     |
| 301         | LNNV                  | SATPK      | CGA       | IS     | DA         | SG          | EL           | S      | A          | E    | GN     | T  | T    | P     |
| 301         | LNNV                  | SATPK      | CGA       | IS     | DA         | SG          | EL           | S      | A          | E    | GN     | T  | T    | P     |
| 301         | LNNV                  | SATPK      | CGA       | IS     | DA         | SG          | EL           | S      | A          | E    | GN     | T  | T    | P     |

|    |     |  |     |
|----|-----|--|-----|
| QY | 361 | TTTELRAAKNHTTFFVDPITTEGETSDVAKINNGSGALANPYOGTTLFSEETLTABELKXA  | 420 |
| Db | 361 | FTTELRAAKNHTTFFVDPITTEGETSDVAKINNGSGALANPYOGTTLFSEETLTABELKXA  | 420 |
| QY | 421 | DNLKSSFTQVPSLSGGKLLLOKGVLTLESTSPFQOAGSLGMDSGTTLSTAGSITITNLG    | 480 |
| Db | 421 | DNLKSSFTQVPSLSGGKLLLOKGVLTLESTSPFQOAGSLGMDSGTTLSTAGSITITNLG    | 480 |
| QY | 481 | INVDLSLGGKQVSLTAKAGSNKVYISGKLNLDIEGNITYESHMFSDQLFSLKLTIVDAD    | 540 |
| Db | 481 | INVDLSLGGKQVSLTAKAGSNKVYISGKLNLDIEGNITYESHMFSDQLFSLKLTIVDAD    | 540 |
| QY | 541 | VDINVDISLLVPVPAEDPNSEXGFOGQNNVMTTDTATNYKEATATWTCTGCVSPERKS     | 600 |
| Db | 541 | VDINVDISLLVPVPAEDPNSEXGFOGQNNVMTTDTATNYKEATATWTCTGCVSPERKS     | 600 |
| QY | 601 | ALVCTNLGCVFTDIRSLLOQLVEIGATGMBKQGFVWSMTNTEFLHKTGDENRKGRHTSGG   | 660 |
| Db | 601 | ALVCTNLGCVFTDIRSLLOQLVEIGATGMBKQGFVWSMTNTEFLHKTGDENRKGRHTSGG   | 660 |
| QY | 661 | YVIGGSATTPKDDLTTFAPCHLPADKOCFLAHNNSRTYGGTLFRKSHITLOPONTLRIG    | 720 |
| Db | 661 | YVIGGSATTPKDDLTTFAPCHLPADKOCFLAHNNSRTYGGTLFRKSHITLOPONTLRIG    | 720 |
| QY | 721 | RAKFSESAIEKPRRIPLALDVQVSFSSDNMETHYSLPSESEGSMECIAGGIGLDL        | 780 |
| Db | 721 | RAKFSESAIEKPRRIPLALDVQVSFSSDNMETHYSLPSESEGSMECIAGGIGLDL        | 780 |
| QY | 781 | PFLVLSNPHPLFXTFLPQMKVEMVYVYSONSFPESSDGRGFSIGRLNLNLSIPVGAKEVQGD | 840 |
| Db | 781 | PFLVLSNPHPLFXTFLPQMKVEMVYVYSONSFPESSDGRGFSIGRLNLNLSIPVGAKEVQGD | 840 |
| QY | 841 | IGDSTTYDLSCGFVSDVYRANPQSTATLYMSQDSMKIRGNLSRQAFLLRGSNNTYYNSN    | 900 |
| Db | 841 | IGDSTTYDLSCGFVSDVYRANPQSTATLYMSQDSMKIRGNLSRQAFLLRGSNNTYYNSN    | 900 |
| QY | 901 | CELFGHYAMELGGSSRNNTVDGCTLRF 928                                |     |
| Db | 901 | CELFGHYAMELGGSSRNNTVDGCTLRF 928                                |     |

| QY  | Result 2   | OS16J7_CHLAB                            | PRT; 1024 AA. |
|---|--|---|---------------|
| AC  | OS16J7_CHLAB   | PRELIMINARY;                            |               |
| DT  | 01-FEB-2005  | (TREMBlrel. 29, Created)                |               |
| DT  | 01-FEB-2005  | (TREMBlrel. 29, Last sequence update)   |               |
| DE  | 01-FEB-2005  | (TREMBlrel. 29, Last annotation update) |               |
| GN  | Name=pmp7G; OrderedlocusNames=CAB269;                                |   |               |
| OS  | Chlamydophila abortus.   |   |               |
| OX  | Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.    |   |               |
| NCBI_TaxId=83555;   |  |   |               |
| RP  | NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].                       |   |               |
| RC  | STRAIN=526/3;  |   |               |
| RA  | PubMed:15637807; DOI=10.1101/gr.3684805;                             |   |               |
| RA  | Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,        |   |               |
| RA  | Livingstone M., Cerdano-Tarraga A.-M., Harris B., Doggett J.,        |   |               |
| RA  | Ormond D., Mungall K., Clarke K., Feltwell T., Hance Z., Sanders M., |   |               |
| RA  | Quail M.A., Pritch C., Barrall B.G., Parkhill J., Lombotom D.;       |   |               |
| RT  | "The Chlamydophila abortus genome sequence reveals an array of       |   |               |
| RT  | variable proteins that contribute to interspecies variation.";       |   |               |
| RL  | Genome Res. 15:629-640(2005) .                                       |   |               |
| KW  | EMBL; CR848038; CAH63725.1; -; Genomic DNA.                          |   |               |
| KW  | Complete proteome.   |   |               |
| SQ  | SEQUENCE 1024 AA; 108663 MW; 268B61415C8FD434 CCR64;                 |   |               |
| Query Match   | 1.5%; Score 14; DB 2; Length 1024;                                   |   |               |
| Best Local Similarity                                       | 100.0%; Fold. No. 0.00022;   |   |               |
| Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |  |   |               |



Db 702 ATWTKGTFVSPSPR 715

## RESULT 3

P71134.CHLAB PRELIMINARY; PRT; 649 AA.  
 AC P71134;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative outer membrane protein (Fragment).  
 OS Chlamydia abortus.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 NCBI\_TaxID=83555;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.,  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U72499; AAB18187.1; -; Genomic DNA.  
 DR GO; GO:0019867; C:outer membrane; IEA.  
 DR InterPro; IPR006315; Autotransporter.  
 DR InterPro; IPR005546; Auto\_transpbeta.  
 DR InterPro; IPR011427; ChlamPMP\_M.  
 DR Pfam; PF03797; Autotransporter; 1.  
 DR Pfam; PF07548; ChlamPMP\_M; 1.  
 DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 649 AA; 70091 MW; 13747C68066A7F50 CRC64;

Query Match 1.3%; Score 12; DB 2; Length 649;  
 Best Local Similarity 100.0%; Pred. No. 0.017;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNVD 921  
 Db 631 ELRGSSRNVD 642

## RESULT 4

Q9RB71.CHLPN PRELIMINARY; PRT; 772 AA.  
 AC Q9RB71; Q7BX22;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Pmp\_3 (Outer membrane protein 5).  
 GN Name=pmp\_3.2; OrderedlocusNames=CpB0018;  
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 NCBI\_TaxID=83558;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA STRAIN=J138;  
 RL MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;  
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.,  
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
 from Japan and Cw1029 from USA."  
 Nucleic Acids Res. 28:2311-2314(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=TW-183;  
 RA Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,  
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.,  
 RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with  
 other Chlamydia strains based on whole genome sequence analysis."  
 Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BA000008; BAA98226.1; -; Genomic DNA.  
 DR EMBL; AE017157; AAP97951.1; -; Genomic DNA.  
 DR PIR; H86492; H86492.  
 DR GO; GO:0019867; C:outer membrane; IEA.  
 DR InterPro; IPR006315; Autotransporter.

DR InterPro; IPR005546; Auto\_transpbeta.  
 DR InterPro; IPR011427; ChlamPMP\_M.  
 DR InterPro; IPR003368; Chlamydia\_PMP.  
 DR Pfam; PF03797; Autotransporter; 1.  
 DR Pfam; PF07548; ChlamPMP\_M; 1.  
 DR Pfam; PF02415; Chlam\_PMP; 6.  
 DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
 DR TIGRFAMs; TIGR01376; POMP\_repeat; 6.  
 SQ SEQUENCE 772 AA; 82931 MW; 484FC56D635801EB CRC64;

Query Match 1.3%; Score 12; DB 2; Length 772;  
 Best Local Similarity 100.0%; Pred. No. 0.02;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNVD 921  
 Db 754 ELRGSSRNVD 765

## RESULT 5

O5L6J2.CHLAB PRELIMINARY; PRT; 1378 AA.  
 AC O5L6J2;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Polymorphic outer membrane protein.  
 GN Name=pmp15G; Synonyms=pomp145A; OrderedlocusNames=CMB283;  
 OS Chlamydia abortus.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 NCBI\_TaxID=83555;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RA STRAIN=826/3;  
 RX PubMed=15837807; DOI=10.1101/gr.3684805;  
 RA Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,  
 RA Livingstone M., Cerdeno-Tarraga A.-M., Harris B., Doggett J.,  
 RA Ormond D., Mungall K., Clarke K., Felwell T., Hance Z., Sanders M.,  
 RA Quail M.A., Price C., Barrett B.G., Parkhill J., Longbottom D.,  
 RT "The Chlamydia abortus genome sequence reveals an array of  
 RT variable proteins that contribute to interspecies variation."  
 RL Genome Res. 15:629-640(2005).  
 DR EMBL; CR848038; CAH63733.1; -; Genomic DNA.  
 KW Complete proteome.

Query Match 1.3%; Score 12; DB 2; Length 1378;  
 Best Local Similarity 100.0%; Pred. No. 0.034;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNVD 921  
 Db 1360 ELRGSSRNVD 1371

## RESULT 6

O8VHT7.CHLPN PRELIMINARY; PRT; 252 AA.  
 AC O8VHT7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Putative polymorphic membrane protein (Fragment).  
 OS Chlamydia psittaci (Chlamydia psittaci).  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 NCBI\_TaxID=83554;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=LLG, and POS;  
 RA Laroucau K., Souriau A., Rodolakis A.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF243413; AAL36957.1; -; Genomic DNA.  
 DR EMBL; AF243414; AAL36958.1; -; Genomic DNA.

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DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF02415; Chlam_PMP; 3.
DR Trifam; TIGR01376; POMP_repat; 3.
FT NOW TRR 252
SQ SEQUENCE 252 AA; 26107 MW; 433CD4F765427318 CRC64;

Query Match
Best Local Similarity 1.1%; Score 10; DB 2; Length 252;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TDNLTPFLGNG 88
DB 81 TDNLTPFLGNG 90

RESULT 7
Q7VQ99_CHLPN PRELIMINARY; PRT; 445 AA.
ID Q7VQ99_CHLPN PRELIMINARY; PRT; 445 AA.
AC Q7VQ99;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Outer membrane protein 5.
GN OrderedLocustNames=CPB0023;
OC Chlamydia pneumoniae (Chlamydiales; Chlamydiaceae; Chlamydia).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TW-183;
RA Geng M.M., Schuhmacher A., Muehlhofer I., Bensch K.W., Schaefer K.P.,
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT other Chlamydia strains based on whole genome sequence analysis.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017157; AA97956.1; -; Genomic_DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR006315; AutoTransporter.
DR InterPro; IPR005546; AutoTransporter.
DR InterPro; IPR011427; ChlamPMP_M.
DR Pfam; PF03797; AutoTransporter; 1.
DR Pfam; PF07548; ChlamPMP_M; 1.
DR Trifam; TIGR01414; autoTrans_bar1; 1.
SQ SEQUENCE 445 AA; 49365 MW; EPA25B0C90A08AA6 CRC64;

Query Match
Best Local Similarity 1.1%; Score 10; DB 2; Length 445;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNYN 919
DB 427 ELRGSSRNYN 436

RESULT 8
Q9RB67_CHLPN PRELIMINARY; PRT; 445 AA.
ID Q9RB67_CHLPN PRELIMINARY; PRT; 445 AA.
AC Q9RB67;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Pmp_5.
GN Name=pmp_5.2;
OC Chlamydia pneumoniae (Chlamydiales; Chlamydiaceae; Chlamydia).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83558;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=J138;
RA MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hatori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138

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RT from Japan and CWI029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; BA000008; BA98231.1; -; Genomic_DNA.
DR PIR; E86493; E86493.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR006315; AutoTransporter.
DR InterPro; IPR005546; AutoTransporter.
DR InterPro; IPR011427; ChlamPMP_M.
DR Pfam; PF03797; AutoTransporter; 1.
DR Pfam; PF07548; ChlamPMP_M; 1.
DR Trifam; TIGR01414; autoTrans_bar1; 1.
SQ SEQUENCE 445 AA; 49353 MW; EPA24AFC9C5097A6 CRC64;

Query Match
Best Local Similarity 1.1%; Score 10; DB 2; Length 445;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNYN 919
DB 427 ELRGSSRNYN 436

RESULT 9
P77792_CHLAB PRELIMINARY; PRT; 839 AA.
ID P77792_CHLAB PRELIMINARY; PRT; 839 AA.
AC P77792; Q5LSP5;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE POMP90B precursor (POMP90A precursor) (Polymorphic outer membrane
DE protein).
GN Name=pmp17g; Synonyms=pomp90B; OrderedLocustNames=CAB598;
OC Chlamydia abortus.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83555;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S26/3;
RA MEDLINE=98187897; PubMed=9529048;
RA Longbottom D., Russell M., Dunbar S.M., Jones G.E., Herring A.J.;
RT "Molecular cloning and characterization of the genes coding for the
RT highly immunogenic cluster of 90-kilodalton envelope proteins from the
RT Chlamydia psittaci subtype that causes abortion in sheep.";
RL Infect. Immun. 66:1317-1324(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S26/3;
RA MEDLINE=96406378; PubMed=8810511; DOI=10.1016/0378-1097(96)00281-9;
RA Longbottom D., Russell M., Jones G.E., Latinson F.A., Herring A.J.;
RT "Identification of a multigene family coding for the 90 kDa proteins
RT of the ovine abortion subtype of Chlamydia psittaci.";
RL FEMS Microbiol. Lett. 142:277-281(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S26/3;
RA PubMed=15837807; DOI=10.1101/gr.3684805;
RA Thomson N.R., Yeats C., Bell K., Holden M.T.G., Bentley S.D.,
RA Livingstone M., Cerdano-Tarraga A.M., Harris B., Doggett J.,
RA Ormond D., Mungall K., Clarke K., Fellwell T., Hance Z., Sanders M.,
RA Quail M.A., Price C., Barrett B.G., Parkhill J., Longbottom D.,
RT "The Chlamydia abortus genome sequence reveals an array of
RT variable proteins that contribute to interspecies variation.";
RL Genome Res. 15:629-640(2005).
DR EMBL; U65943; AAC15922.1; -; Genomic_DNA.
DR EMBL; U65943; AAC15922.1; -; Genomic_DNA.
DR EMBL; CR848038; CAH64045.1; -; Genomic_DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR005546; AutoTransporter.
DR InterPro; IPR006315; AutoTransporter.
DR InterPro; IPR011427; ChlamPMP_M.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; AutoTransporter; 1.
DR Pfam; PF02415; Chlam_PMP; 4.

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DR Pfam; PF07548; ChlAMP\_M; 1.  
 DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
 DR TIGRFAMs; TIGR01376; POMP\_repeat; 3.  
 KM Complete proteome; Signal.  
 FT SIGNAL 1 16 Potential.  
 FT CHAIN 17 839 POMP90B.  
 SQ SEQUENCE 839 AA; 89825 MW; 4581C7CBAF7FFA4C CRC64;

Query Match 1.1%; Score 10; DB 2; Length 839;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TDNLTFKNG 88  
 |||||  
 Db 81 TDNLTFKNG 90

RESULT 10  
 Q9PZ1\_XYLFA PRELIMINARY; PRT; 261 AA.  
 AC Q9PZ1;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocustNames=Xf0515;  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xylella.  
 OX NCBI\_TaxID=2371;  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=945C;  
 RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carriro D.M., Carver H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Facincani A.P., Ferreira A.U.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
 RA Garner M., Goldman G.H., Goldman H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
 RA Krieger J.E., Kurana E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins B.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Faria A.,  
 RA Paixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,  
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA da Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva M.A. Jr.,  
 RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
 RA de Souza A.P., Terezzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,  
 RA Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., Secubal J.C.  
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*."  
 RL Nucleic Acids Res. 31:151-159(2003).  
 DR EMBL: A600390; A603325.1; -; Genomic\_DNA.  
 DR PIR: F82795; F82795.  
 KM Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 261 AA; 30007 MW; AC8E80B886D406E CRC64;

Query Match 1.0%; Score 9; DB 2; Length 261;  
 Best Local Similarity 100.0%; Pred. No. 9.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 532 LKITYDAD 540  
 |||||

Db 4 LKITYDAD 12

RESULT 11  
 Q7NHT5\_GLOVI PRELIMINARY; PRT; 337 AA.  
 AC Q7NHT5;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Glr250 protein.  
 GN OrderedLocustNames=g1r2450;  
 OS Gloeobacter violaceus.  
 OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacter.  
 OX NCBI\_TaxID=33072;  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RP STRAIN=PCC 7421;  
 RC MEDLINE=22977040; PubMed=14621292;  
 RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,  
 RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,  
 RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S.,  
 RA Takeuchi C., Yamada M., Tabata S.,  
 RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a  
 cyanobacterium that lacks thylakoids."  
 RL DNA Res. 10:137-145(2003).  
 DR EMBL: BA000045; BAC90391.1; -; Genomic\_DNA.  
 DR HSP: P4169; IOR.  
 DR GO: GO:0003824; F:catalytic activity; IEA.  
 DR GO: GO:0051287; F:NAD binding; IEA.  
 DR GO: GO:0009225; P:nucleotide-sugar metabolism; IEA.  
 DR InterPro: IPR001509; Epimerase\_Dh.  
 DR Pfam: PF01370; Epimerase; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 337 AA; 36521 MW; 3C1B295585AEC94F CRC64;

Query Match 1.0%; Score 9; DB 2; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 GAKFVGDI 841  
 |||||  
 Db 57 GAKFVGDI 65

RESULT 12  
 Q6W3N9\_9PROT PRELIMINARY; PRT; 475 AA.  
 AC Q6W3N9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE UDP-murNac-pentapeptide presynthetase.  
 GN Name=murF;  
 OS *Alvinella pompejana* epibiont 6C6.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria.  
 OX NCBI\_TaxID=244799;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=22837667; PubMed=12957888;  
 RX DOI=10.1128/AEM.69.9.5070-5078.2003;  
 RA Campbell B.J., Stein J.L., Cary S.C.;  
 RT "Evidence of chemolithoautotrophy in the bacterial community  
 associated with *Alvinella pompejana*, a hydrothermal vent polychaete."  
 RL Appl. Environ. Microbiol. 69:5070-5078(2003).  
 DR EMBL: AY312990; AAQ75142.1; -; Genomic\_DNA.  
 DR GO: GO:0005524; P:ATP binding; IEA.  
 DR GO: GO:0016874; P:ligase activity; IEA.  
 DR GO: GO:0009058; P:biosynthesis; IEA.  
 DR InterPro: IPR004101; Mur\_ligase\_C.  
 DR InterPro: IPR012237; UDP-NACM\_Alig.  
 DR Pfam: PF02875; Mur\_ligase\_C; 1.  
 DR PIRSF: PIRSF001562; UDP-NACM\_Alig; 1.

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SQ SEQUENCE 475 AA; 54554 MW; B6F5F2301CAFLCDD CRC64;
Query Match 1.0%; Score 9; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 32 DDFRNGID 40
    |||||
Db 369 DDFRNGID 377

RESULT 13
YMA2_YEAST STANDARD; PRT; 737 AA.
ID YMA2_YEAST
AC Q04263; Q03665;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical 84.6 kDa protein in GLO1-IPF7 intergenic region.
GN OrderedLocustNames=YML002W; ORFNames=YM9571.17, YM8270.01;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagsis K., Lyne G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S.V., Whitehead S., Barrett B.G.,
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; Z49810; CAA89950.1; -; Genomic_DNA.
CC EMBL; Z48613; CAA88514.1; -; Genomic_DNA.
CC PIR; S55117; S55117.
CC GerMOnline; 142532; -.
CC DR Ensembl; YML002W; Saccharomyces cerevisiae.
CC SGP; S000004461; YML002W.
CC InterPro; IPR002110; ANK.
CC DR SMART; SM00248; ANK; 3.
CC KM Complete proteome; Hypothetical protein.
CC SQ SEQUENCE 737 AA; 84602 MW; 563B6B6A073657C CRC64;

Query Match 1.0%; Score 9; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 183 FSNSSSTK 191
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Db 48 FSNSSSTK 56

RESULT 14
O6B2L5_YEAST PRELIMINARY; PRT; 737 AA.
ID O6B2L5_YEAST
AC O6B2L5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE YML002W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

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OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Marschick G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA Labaer J.;
RT "Creation of the YFLEX clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY92715; AY92734.1; -; Genomic_DNA.
DR Ensembl; YML002W; Saccharomyces cerevisiae.
DR SGP; S000004461; YML002W.
DR InterPro; IPR002110; ANK.
SQ SEQUENCE 737 AA; 84533 MW; 4592E329948375B3 CRC64;

Query Match 1.0%; Score 9; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 183 FSNSSSTK 191
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Db 48 FSNSSSTK 56

RESULT 15
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ID O823X4_CHLCV PRELIMINARY; PRT; 868 AA.
AC O823X4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polymorphic outer membrane protein G family protein.
GN OrderedLocustNames=CCA00279;
OS Chlamydia caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=33557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SPRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J.F., Holtzapfele B.K., Khouri H.M., Federova N.B.,
RA Carthy H.A., Umayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,
RA White O., Salzberg S.L., Heia R.-C., McClarty G., Rank R.G.,
RA Bavoil P.M., Fraser C.M.;
RT "Genome sequence of Chlamydia caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae."
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AE016995; AAP05030.1; -; Genomic_DNA.
DR TIGR; CCA00279; -.
DR GO; GO:0019867; C:outer membrane, IEA.
DR InterPro; IPR005546; Auto_transpbeta.
DR InterPro; IPR003368; Chlamydia_PMP.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF07548; ChlamPMP_M; 1.
DR Pfam; PF02415; Chlam_PMP; 3.
DR TIGRFAMs; TIGR01376; POMP_repeat; 1.
DR Complete proteome.
SQ SEQUENCE 868 AA; 96015 MW; 52918F69F4FD3FF4 CRC64;

Query Match 1.0%; Score 9; DB 2; Length 868;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 653 GFRITSGY 661
    |||||
Db 592 GFRITSGY 600

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Mon Nov 28 09:39:52 2005

us-09-446-677b-2.011.rup

Page 7

Search completed: November 25, 2005, 14:46:24  
Job time : 144.29 secs

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OM protein - protein search, using sw model

Run on: November 25, 2005, 14:24:03 ; Search time 27.6938 Seconds  
(without alignments)  
2770.401 Million cell updates/sec

Title: US-09-446-677B-2

Perfect score: 928

Sequence: 1 MKTSLPWLVSVAFLAFSCHL.....MELRGSSRNVDVGTGRF 928

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5.COMB.dep:\*  
2: /cgn2\_6/prodata/1/aa/6.COMB.dep:\*  
3: /cgn2\_6/prodata/1/aa/H.COMB.dep:\*  
4: /cgn2\_6/prodata/1/aa/PTUS.COMB.dep:\*  
5: /cgn2\_6/prodata/1/aa/RS.COMB.dep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.dep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | length | DB ID | Description          |
|------------|-------|-------------|--------|-------|----------------------|
| 1          | 928   | 100.0       | 967    | 2     | US-09-438-185A-453   |
| 2          | 827   | 89.1        | 949    | 2     | US-09-198-452A-478   |
| 3          | 12    | 1.3         | 230    | 2     | US-09-198-452A-30    |
| 4          | 12    | 1.3         | 780    | 2     | US-09-438-185A-17    |
| 5          | 12    | 1.3         | 928    | 2     | US-09-428-122-2      |
| 6          | 10    | 1.1         | 450    | 2     | US-09-198-452A-35    |
| 7          | 10    | 1.1         | 450    | 2     | US-09-438-185A-21    |
| 8          | 9     | 1.0         | 930    | 2     | US-09-198-452A-470   |
| 9          | 9     | 1.0         | 938    | 2     | US-09-438-185A-448   |
| 10         | 9     | 0.9         | 76     | 2     | US-09-583-110-4935   |
| 11         | 8     | 0.9         | 76     | 2     | US-09-107-433-3629   |
| 12         | 8     | 0.9         | 117    | 2     | US-09-270-767-57096  |
| 13         | 8     | 0.9         | 139    | 2     | US-09-540-236-3194   |
| 14         | 8     | 0.9         | 201    | 2     | US-09-270-767-33568  |
| 15         | 8     | 0.9         | 201    | 2     | US-09-270-767-33568  |
| 16         | 8     | 0.9         | 218    | 2     | US-09-249-180-6      |
| 17         | 8     | 0.9         | 295    | 2     | US-09-248-796A-14734 |
| 18         | 8     | 0.9         | 335    | 2     | US-09-270-767-41852  |
| 19         | 8     | 0.9         | 335    | 2     | US-09-248-796A-14735 |
| 20         | 8     | 0.9         | 427    | 2     | US-09-198-452A-31    |
| 21         | 8     | 0.9         | 458    | 2     | US-09-542-520-36     |
| 22         | 8     | 0.9         | 458    | 2     | US-09-542-520-36     |
| 23         | 8     | 0.9         | 505    | 2     | US-09-612-402B-17    |
| 24         | 8     | 0.9         | 505    | 2     | US-09-542-520-17     |
| 25         | 8     | 0.9         | 522    | 2     | US-09-198-452A-480   |
| 26         | 8     | 0.9         | 530    | 2     | US-09-198-452A-482   |
| 27         | 8     | 0.9         | 597    | 2     | US-09-198-452A-29    |

|    |   |     |      |   |                    |                   |
|----|---|-----|------|---|--------------------|-------------------|
| 28 | 8 | 0.9 | 602  | 2 | US-09-438-185A-18  | Sequence 18, Appl |
| 29 | 8 | 0.9 | 634  | 2 | US-09-438-185A-451 | Sequence 451, App |
| 30 | 8 | 0.9 | 643  | 2 | US-09-198-452A-474 | Sequence 474, App |
| 31 | 8 | 0.9 | 670  | 2 | US-10-197-220-169  | Sequence 169, App |
| 32 | 8 | 0.9 | 922  | 2 | US-09-198-452A-15  | Sequence 15, Appl |
| 33 | 8 | 0.9 | 932  | 2 | US-09-438-185A-6   | Sequence 6, Appl1 |
| 34 | 8 | 0.9 | 973  | 2 | US-09-430-723-2    | Sequence 2, Appl1 |
| 35 | 8 | 0.9 | 982  | 2 | US-09-556-877-176  | Sequence 176, App |
| 36 | 8 | 0.9 | 982  | 2 | US-09-620-412C-176 | Sequence 176, App |
| 37 | 8 | 0.9 | 982  | 2 | US-09-598-419-176  | Sequence 176, App |
| 38 | 8 | 0.9 | 984  | 2 | US-09-612-402B-43  | Sequence 43, Appl |
| 39 | 8 | 0.9 | 999  | 2 | US-09-438-185A-455 | Sequence 455, App |
| 40 | 8 | 0.9 | 1006 | 2 | US-09-556-877-190  | Sequence 190, App |
| 41 | 8 | 0.9 | 1006 | 2 | US-09-620-412C-190 | Sequence 190, App |
| 42 | 8 | 0.9 | 1006 | 2 | US-09-598-419-190  | Sequence 190, App |
| 43 | 8 | 0.9 | 1012 | 2 | US-09-612-402B-2   | Sequence 2, Appl1 |
| 44 | 8 | 0.9 | 1012 | 2 | US-09-542-520A-2   | Sequence 2, Appl1 |
| 45 | 8 | 0.9 | 1013 | 2 | US-09-612-402B-15  | Sequence 15, Appl |

#### ALIGNMENTS

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RESULT 1
US-09-438-185A-453
; Sequence 453, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438, 185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108, 279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128, 606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 453
; LENGTH: 967
; TYPE: PR
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0451
US-09-438-185A-453
Query Match 100.0%; Score 928; DB 2; Length 967;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKTSLPWLVSVAFLAFSCHLQSLANEELSPDSEFNGNIDSGTFPEPKATATYSLTGDF 60
40 MKTSLPWLVSVAFLAFSCHLQSLANEELSPDSEFNGNIDSGTFPEPKATATYSLTGDF 99
61 FPEPKATATYSLTGDF 120
121 LSPDSEFNGNIDSGTFPEPKATATYSLTGDF 180
160 LSPDSEFNGNIDSGTFPEPKATATYSLTGDF 219
181 LSPDSEFNGNIDSGTFPEPKATATYSLTGDF 240
220 LSPDSEFNGNIDSGTFPEPKATATYSLTGDF 279
241 LSPDSEFNGNIDSGTFPEPKATATYSLTGDF 300
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Dh 280 EGNAAKTTGGAICNTKASGSPELLIISNNKTLIFASVAETSGAIIHAKKULALSSGGFTEF 339  
Qy 301 LRNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKNAINIGSNGK 360  
Db 340 LRNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKNAINIGSNGK 399  
Qy 361 FTBLRAAKNHTIFPYDPTISEGSSDVLKINNSAGALNPYQGTILFSGETLTADBLKVA 420  
Db 400 FTBLRAAKNHTIFPYDPTISEGSSDVLKINNSAGALNPYQGTILFSGETLTADBLKVA 459  
Qy 421 DNKSSFTQPVLSLGGKLLLOKGVLTSTSPQASGLIGMDSGTTLSTAAGSTTTNIG 480  
Db 460 DNKSSFTQPVLSLGGKLLLOKGVLTSTSPQASGLIGMDSGTTLSTAAGSTTTNIG 519  
Qy 481 INVDLGLKOPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540  
Db 520 INVDLGLKOPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 579  
Qy 541 VDTNVDISSLIPVPAEDPNSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 600  
Db 580 VDTNVDISSLIPVPAEDPNSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 639  
Qy 601 ALVNTLMGVPTDRLSLQOLVEIGATGMEHKQGFWSMNTFLHKTGDENRKGRHTSGG 660  
Db 640 ALVNTLMGVPTDRLSLQOLVEIGATGMEHKQGFWSMNTFLHKTGDENRKGRHTSGG 699  
Qy 661 YVIGSAHTPKDGLFTFAFCHLPARDKDCFIAHNSRTYGGTLFPKHSHTLQPNYLRLG 720  
Db 700 YVIGSAHTPKDGLFTFAFCHLPARDKDCFIAHNSRTYGGTLFPKHSHTLQPNYLRLG 759  
Qy 721 RAKFSESAIEKPREIPLADVOVSFSHSDNRMETHYTSLPESGWSNECICIGLDL 780  
Db 760 RAKFSESAIEKPREIPLADVOVSFSHSDNRMETHYTSLPESGWSNECICIGLDL 819  
Qy 781 PFLVSNHPLKFTIIPQMKVEMVYVSONSPFESSSDRGSGISGRLLNLSTIPVGAKFVQGD 840  
Db 820 PFLVSNHPLKFTIIPQMKVEMVYVSONSPFESSSDRGSGISGRLLNLSTIPVGAKFVQGD 879  
Qy 841 IGDSTYDLSGFPVSDVYRNNPOSTATLVMSPSWKIRGMLSRQAFLLRGSNNVYVNSN 900  
Db 880 IGDSTYDLSGFPVSDVYRNNPOSTATLVMSPSWKIRGMLSRQAFLLRGSNNVYVNSN 939  
Qy 901 CELFGHYAMELRGSSRNYNVDVGTCLRF 928  
Db 940 CELFGHYAMELRGSSRNYNVDVGTCLRF 967

## RESULT 2

US-09-198-452A-478  
; Sequence 478, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griflais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 478  
; LENGTH: 949  
; TYPE: PR1  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: 1...949  
; OTHER INFORMATION: Xaa=unknown or other  
US-09-198-452A-478

Query Match 89.1%; Score 827; DB 2; Length 949;  
Best Local Similarity 99.9%; Fred. No. 0;  
Matches 927; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKTISPMVLVSSVLAFSCHLQSLANBELLSPDSEFNGNIDSGTFPTKTSATTYSLTGDF 60  
Db 22 MKTISPMVLVSSVLAFSCHLQSLANBELLSPDSEFNGNIDSGTFPTKTSATTYSLTGDF 81  
Qy 61 FYEPGKGTPLSDSCFCQTTDNLTLFLNGHSLTFPGFIDACTHGAASSTANKRLTFSGFS 120  
Db 82 FYEPGKGTPLSDSCFCQTTDNLTLFLNGHSLTFPGFIDACTHGAASSTANKRLTFSGFS 141  
Qy 121 LLSFDSSTPTVTTGGATLSSAGVNLNIRKLVAGNESTADGCAIKGASFLTLTSGD 180  
Db 142 LLSFDSSTPTVTTGGATLSSAGVNLNIRKLVAGNESTADGCAIKGASFLTLTSGD 201  
Qy 181 ALFSNNSSSTKGAIAITTAGARIANNTRYVRLSNIASTSGAIDEGRSILSNKFLYF 240  
Db 202 ALFSNNSSSTKGAIAITTAGARIANNTRYVRLSNIASTSGAIDEGRSILSNKFLYF 261  
Qy 241 EGNAAKTTGGAICNTKASGSPELLIISNNKTLIFASVAETSGAIIHAKKULALSSGGFTEF 300  
Db 262 EGNAAKTTGGAICNTKASGSPELLIISNNKTLIFASVAETSGAIIHAKKULALSSGGFTEF 321  
Qy 301 LRNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKNAINIGSNGK 360  
Db 322 LRNVSSATPKGGAISIDASGELSLSAETGNITFVRNTLTGTTGSTDTPKNAINIGSNGK 381  
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Db 382 FTBLRAAKNHTIFPYDPTISEGSSDVLKINNSAGALNPYQGTILFSGETLTADBLKVA 441  
Qy 421 DNKSSFTQPVLSLGGKLLLOKGVLTSTSPQASGLIGMDSGTTLSTAAGSTTTNIG 480  
Db 442 DNKSSFTQPVLSLGGKLLLOKGVLTSTSPQASGLIGMDSGTTLSTAAGSTTTNIG 501  
Qy 481 INVDLGLKOPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 540  
Db 502 INVDLGLKOPVSLTAKGASNKVIVSGKLNLDIEGNIYESHMFSDQLFSLKITYDAD 561  
Qy 541 VDTNVDISSLIPVPAEDPNSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 600  
Db 562 VDTNVDISSLIPVPAEDPNSEYFGQGMNVNMTTDTATNTKEATATWTGTGFPVSPERKS 621  
Qy 601 ALVNTLMGVPTDRLSLQOLVEIGATGMEHKQGFWSMNTFLHKTGDENRKGRHTSGG 660  
Db 622 ALVNTLMGVPTDRLSLQOLVEIGATGMEHKQGFWSMNTFLHKTGDENRKGRHTSGG 681  
Qy 661 YVIGSAHTPKDGLFTFAFCHLPARDKDCFIAHNSRTYGGTLFPKHSHTLQPNYLRLG 720  
Db 682 YVIGSAHTPKDGLFTFAFCHLPARDKDCFIAHNSRTYGGTLFPKHSHTLQPNYLRLG 741  
Qy 721 RAKFSESAIEKPREIPLADVOVSFSHSDNRMETHYTSLPESGWSNECICIGLDL 780  
Db 742 RAKFSESAIEKPREIPLADVOVSFSHSDNRMETHYTSLPESGWSNECICIGLDL 801  
Qy 781 PFLVSNHPLKFTIIPQMKVEMVYVSONSPFESSSDRGSGISGRLLNLSTIPVGAKFVQGD 840  
Db 802 PFLVSNHPLKFTIIPQMKVEMVYVSONSPFESSSDRGSGISGRLLNLSTIPVGAKFVQGD 861  
Qy 841 IGDSTYDLSGFPVSDVYRNNPOSTATLVMSPSWKIRGMLSRQAFLLRGSNNVYVNSN 900  
Db 862 IGDSTYDLSGFPVSDVYRNNPOSTATLVMSPSWKIRGMLSRQAFLLRGSNNVYVNSN 921  
Qy 901 CELFGHYAMELRGSSRNYNVDVGTCLRF 928  
Db 922 CELFGHYAMELRGSSRNYNVDVGTCLRF 949

## RESULT 3

US-09-198-452A-30  
; Sequence 30, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griflais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments



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; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 30
; LENGTH: 230
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-30

Query Match
Best Local Similarity 1.3%; Score 12; DB 2; Length 230;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYVD 921
Db 212 ELRGSSRNRYVD 223

RESULT 4
US-09-438-185A-17
; Sequence 17, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 780
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0015
US-09-438-185A-17

Query Match
Best Local Similarity 1.3%; Score 12; DB 2; Length 780;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYVD 921
Db 762 ELRGSSRNRYVD 773

RESULT 5
US-09-428-122-2
; Sequence 2, Application US/09428122
; Patent No. 6872814
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
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; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-09-428-122-2

Query Match
Best Local Similarity 1.3%; Score 12; DB 2; Length 928;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYVD 921
Db 910 ELRGSSRNRYVD 921

RESULT 6
US-09-198-452A-35
; Sequence 35, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 35
; LENGTH: 450
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-35

Query Match
Best Local Similarity 1.1%; Score 10; DB 2; Length 450;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYN 919
Db 432 ELRGSSRNRYN 441

RESULT 7
US-09-438-185A-21
; Sequence 21, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kaiman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 450
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0019
US-09-438-185A-21
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Query Match 1.1%; Score 10; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYN 919  
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Db 432 ELRGSSRNRYN 441

## RESULT 8

US-09-198-452A-470  
; Sequence 470, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 470  
; LENGTH: 930  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-470

Query Match 1.0%; Score 9; DB 2; Length 930;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AGAASTTA 110  
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Db 107 AGAASTTA 115

## RESULT 9

US-09-438-185A-448  
; Sequence 448, Application US/09438185A  
; Patent No. 6822071  
; GENERAL INFORMATION:  
; APPLICANT: Stephens, Richard  
; APPLICANT: Mitchell, Wayne  
; APPLICANT: Kaiman, Sue  
; APPLICANT: Davis, Ronald  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence  
; FILE REFERENCE: 018941-000411US  
; CURRENT APPLICATION NUMBER: US/09/438,185A  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/108,279  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/128,606  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 1074  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 448  
; LENGTH: 938  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; OTHER INFORMATION: CPH0446  
US-09-438-185A-448

Query Match 1.0%; Score 9; DB 2; Length 938;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AGAASTTA 110  
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Db 115 AGAASTTA 123

RESULT 10  
US-09-583-110-4935  
; Sequence 4935, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucet-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnosis and Therapeutics  
; FILE REFERENCE: PAT00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 4935  
; LENGTH: 76  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-4935

Query Match 0.9%; Score 8; DB 2; Length 76;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 LTADELKV 419  
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Db 25 LTADELKV 32

## RESULT 11

US-09-107-433-3629  
; Sequence 3629, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucet-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 3629:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 76 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;     ORGANISM: Streptococcus pneumoniae
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...76
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3629:
US-09-107-433-3629

Query Match
Best Local Similarity 100.0%; DB 2; Length 76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 LTADELKV 419
Db 25 LTADELKV 32

RESULT 12
US-09-270-767-57096
; Sequence 57096, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 57096
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57096

Query Match
Best Local Similarity 100.0%; DB 2; Length 117;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 NAAKTTGG 250
Db 4 NAAKTTGG 11

RESULT 13
US-09-540-236-3194
; Sequence 3194, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;   APPLICANT: Gary L. Breton et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATRA
;   FILE REFERENCE: 2709.2005-001
;   CURRENT APPLICATION NUMBER: US/09/540,236
;   CURRENT FILING DATE: 2000-04-04
;   NUMBER OF SEQ ID NOS: 3840
;   SEQ ID NO 3194
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: M.catarhalis
US-09-540-236-3194

Query Match
Best Local Similarity 100.0%; DB 2; Length 199;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 744 VFSHSDN 751
Db 83 VFSHSDN 90

RESULT 14
US-09-270-767-33568
; Sequence 33568, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 33568
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-33568

Query Match
Best Local Similarity 100.0%; DB 2; Length 201;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAAASTTA 110
Db 143 GAAASTTA 150

RESULT 15
US-09-270-767-48785
; Sequence 48785, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;   APPLICANT: Homburger et al.
;   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;   FILE REFERENCE: File Reference: 7326-094
;   CURRENT APPLICATION NUMBER: US/09/270,767
;   CURRENT FILING DATE: 1999-03-17
;   NUMBER OF SEQ ID NOS: 62517
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 48785
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-48785

Query Match
Best Local Similarity 100.0%; DB 2; Length 201;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAAASTTA 110
Db 143 GAAASTTA 150

Search completed: November 25, 2005, 14:49:57
Job time : 28.6938 secs
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 25, 2005, 14:30:28 ; Search time 97.9541 Seconds

(without alignments)  
3958.441 Million cell updates/sec

Title: US-09-446-677b-2

Perfect score: 928

Sequence: 1 MKTSLPWLVSVAFLSFCHL.....MELRGSSRYNYDVGTGLR 928

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:

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18: /cgn2\_6/ptodata/1/pubpaa/US24\_PUBCOMB.pep.\*

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Pred. No. is the number of results predicted to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match | Length | DB | ID                   | Description        |
|------------|-------|-------|--------|----|----------------------|--------------------|
| 1          | 928   | 100.0 | 928    | 4  | US-10-312-273-115    | Sequence 115, App  |
| 2          | 928   | 100.0 | 928    | 4  | US-10-282-122A-54681 | Sequence 54681, A  |
| 3          | 827   | 89.1  | 949    | 4  | US-10-289-762-478    | Sequence 478, App  |
| 4          | 12    | 1.3   | 230    | 4  | US-10-289-762-30     | Sequence 30, Appl  |
| 5          | 12    | 1.3   | 746    | 4  | US-10-312-273-19     | Sequence 19, Appl  |
| 6          | 12    | 1.3   | 928    | 3  | US-09-428-122-2      | Sequence 2, Appl   |
| 7          | 10    | 1.1   | 395    | 4  | US-10-312-273-21     | Sequence 21, Appl  |
| 8          | 10    | 1.1   | 450    | 4  | US-10-289-762-35     | Sequence 35, Appl  |
| 9          | 10    | 1.1   | 839    | 4  | US-09-738-269-23     | Sequence 23, Appl  |
| 10         | 10    | 1.1   | 839    | 4  | US-10-023-437-23     | Sequence 23, Appl  |
| 11         | 9     | 1.0   | 930    | 4  | US-10-312-273-45     | Sequence 45, Appl  |
| 12         | 9     | 1.0   | 930    | 4  | US-10-289-762-470    | Sequence 470, App  |
| 13         | 9     | 1.0   | 930    | 4  | US-10-282-122A-54680 | Sequence 54680, A  |
| 14         | 8     | 0.9   | 53     | 4  | US-10-425-115-353071 | Sequence 353071, A |
| 15         | 8     | 0.9   | 76     | 5  | US-10-617-320-3629   | Sequence 3629, Ap  |
| 16         | 8     | 0.9   | 92     | 4  | US-10-437-963-181650 | Sequence 181650, A |
| 17         | 8     | 0.9   | 93     | 4  | US-10-291-265-251    | Sequence 251, App  |
| 18         | 8     | 0.9   | 93     | 4  | US-10-291-265-723    | Sequence 723, App  |
| 19         | 8     | 0.9   | 112    | 4  | US-10-106-698-5720   | Sequence 5720, Ap  |
| 20         | 8     | 0.9   | 140    | 4  | US-10-425-115-272446 | Sequence 272446, A |
| 21         | 8     | 0.9   | 171    | 4  | US-10-425-115-255238 | Sequence 255238, A |
| 22         | 8     | 0.9   | 218    | 3  | US-09-742-137-6      | Sequence 6, Appl   |
| 23         | 8     | 0.9   | 218    | 3  | US-09-742-160A-6     | Sequence 6, Appl   |
| 24         | 8     | 0.9   | 218    | 4  | US-10-310-154-691    | Sequence 691, App  |
| 25         | 8     | 0.9   | 225    | 4  | US-10-425-115-304034 | Sequence 304034, A |
| 26         | 8     | 0.9   | 227    | 4  | US-10-309-804-8      | Sequence 8, Appl   |
| 27         | 8     | 0.9   | 227    | 4  | US-10-391-399-12     | Sequence 12, Appl  |

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| 28 | 8 | 0.9 | 231 | 4 | US-10-425-115-247895 | Sequence 247895, A |
| 29 | 8 | 0.9 | 234 | 3 | US-09-764-875-767    | Sequence 767, App  |
| 30 | 8 | 0.9 | 240 | 4 | US-10-425-115-271893 | Sequence 271893, A |
| 31 | 8 | 0.9 | 267 | 3 | US-09-764-870-359    | Sequence 359, App  |
| 32 | 8 | 0.9 | 267 | 4 | US-10-125-540-359    | Sequence 359, App  |
| 33 | 8 | 0.9 | 312 | 4 | US-10-425-115-67993  | Sequence 67993, A  |
| 34 | 8 | 0.9 | 324 | 4 | US-10-389-566-910    | Sequence 910, App  |
| 35 | 8 | 0.9 | 342 | 4 | US-10-369-499-2885   | Sequence 2885, Ap  |
| 36 | 8 | 0.9 | 427 | 4 | US-10-289-762-31     | Sequence 31, Appl  |
| 37 | 8 | 0.9 | 428 | 4 | US-10-437-963-179295 | Sequence 179295, A |
| 38 | 8 | 0.9 | 432 | 5 | US-10-873-467-60     | Sequence 60, Appl  |
| 39 | 8 | 0.9 | 456 | 4 | US-10-112-944-329    | Sequence 329, App  |
| 40 | 8 | 0.9 | 458 | 4 | US-10-701-844-36     | Sequence 36, Appl  |
| 41 | 8 | 0.9 | 458 | 4 | US-10-766-711-36     | Sequence 36, Appl  |
| 42 | 8 | 0.9 | 458 | 5 | US-10-931-776-36     | Sequence 36, Appl  |
| 43 | 8 | 0.9 | 486 | 3 | US-09-738-628-5629   | Sequence 5629, Ap  |
| 44 | 8 | 0.9 | 499 | 5 | US-10-739-930-8216   | Sequence 8216, Ap  |
| 45 | 8 | 0.9 | 505 | 4 | US-10-701-844-17     | Sequence 17, Appl  |

## ALIGNMENTS

## Result 1

US-10-312-273-115

Sequence 115, Application US/10312273

Publication No. US2004000567A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE

FILE REFERENCE: P025035W0

CURRENT APPLICATION NUMBER: US/10/312,273

PRIOR FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: 0016363.4

PRIOR FILING DATE: 2000-07-03

PRIOR APPLICATION NUMBER: 0017047.2

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 0017983.8

PRIOR FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: 0019368.0

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 0020440.4

PRIOR FILING DATE: 2000-08-18

PRIOR APPLICATION NUMBER: 0022583.9

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 0027549.5

PRIOR FILING DATE: 2000-11-10

PRIOR APPLICATION NUMBER: 0031706.5

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 664

SOFTWARE: SeqWin99, version 1.02

SEQ ID NO 115

LENGTH: 928

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

US-10-312-273-115

Query Match 100.0%; Score 928; DB 4; Length 928;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| DB | 1   | MKTSLPWLVSVAFLSFCHLQSLANEELSPDPSFNGNIDSTFPFKTSATYSLTGDFV  | 60  |
| QY | 61  | FYEPKGTPLSDSCKQTTDNLTFPLNGHSLTFPGIDAGTGAAGAATTTANKTLFSGRS | 120 |
| DB | 61  | FYEPKGTPLSDSCKQTTDNLTFPLNGHSLTFPGIDAGTGAAGAATTTANKTLFSGRS | 120 |
| QY | 121 | LSPFSSSTVTTCGTLSSAGGVNLENIRKLVAAGNFSTADGAIKGAFLTGTSGD     | 180 |
| DB | 121 | LSPFSSSTVTTCGTLSSAGGVNLENIRKLVAAGNFSTADGAIKGAFLTGTSGD     | 180 |

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| | | | |
DB 241 EGNAAKTGGAI CNTAASGSPELII SNKTLIFASVVAETSGAIIHAKKLALSSGGFTF 300
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| | | | |
DB 301 LRNNVSSATPKGAI SIDASGELS SAETGNITFVRNTLTTTGSTDPKRNAINISNGK 360
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DB 361 FTFLRAAKHNTIFFYDPITSEGTSSDVLKINNNSAGALNPYOGTILFSGETTLADELKVA 420
QY 421 DNKSSFTOPVSLSGGKLLQKVTLESTFSQDASGLGMDGTTLLSTTAGSITTTNLG 480
| | | | |
DB 421 DNKSSFTOPVSLSGGKLLQKVTLESTFSQDASGLGMDGTTLLSTTAGSITTTNLG 480
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| | | | |
DB 481 INVDSLGLKQPVSLTKAGSNKTVISGKMLIDIBGNYESHMFSDOLFSLLKITVDAD 540
QY 541 VDTNVDISSLIPVPAEDPNSYGFQOGOMVMTTDTATNTKEATATWTGTGVPSPERKS 600
| | | | |
DB 541 VDTNVDISSLIPVPAEDPNSYGFQOGOMVMTTDTATNTKEATATWTGTGVPSPERKS 600
QY 601 ALVGNLTMGVFTIRSLQQLVEIGATGMEHKQGFVWSMTNPLHKTGDENRKGFRHTSG 660
| | | | |
DB 601 ALVGNLTMGVFTIRSLQQLVEIGATGMEHKQGFVWSMTNPLHKTGDENRKGFRHTSG 660
QY 661 YVIGSAHTPKDOLLTFPAFCHLPARDKCFIAHNSRTYGGTLFFKHSHTLQPNYLRLG 720
| | | | |
DB 661 YVIGSAHTPKDOLLTFPAFCHLPARDKCFIAHNSRTYGGTLFFKHSHTLQPNYLRLG 720
QY 721 RAFFSSAIEKFPREIPLADVOVSFSHSNRMETHYTSLPESGSMNCCIAGGIGL 780
| | | | |
DB 721 RAFFSSAIEKFPREIPLADVOVSFSHSNRMETHYTSLPESGSMNCCIAGGIGL 780
QY 781 PFLSNPHPLPKTFIIPQMKEMYVSGNSFFESSSDRGFSIGLNLISI PVGAKFVQGD 840
| | | | |
DB 781 PFLSNPHPLPKTFIIPQMKEMYVSGNSFFESSSDRGFSIGLNLISI PVGAKFVQGD 840
QY 841 IGDSTYVDSGFPVSDVYRNNPOSTATLVMSPDWSKIRGANLSQAFILRGSNVYVNSN 900
| | | | |
DB 841 IGDSTYVDSGFPVSDVYRNNPOSTATLVMSPDWSKIRGANLSQAFILRGSNVYVNSN 900
QY 901 CELFGHYAMELRGSSRYNNDVGTKLRF 928
| | | | |
DB 901 CELFGHYAMELRGSSRYNNDVGTKLRF 928

RESULT 2
US-10-282-122A-54681
; Sequence 54681, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Twack, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
```

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; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 54681
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54681

Query Match 100.0%; Score 928; DB 4; Length 928;
Best Local Similarity 100.0%; Pred No. 0;
Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKTISIPWLVSSVLAFSCHLQSLANBELLSPDDSPFNIGDGTFTPKTSATTYSLTGDYF 60
| | | | |
DB 1 MKTISIPWLVSSVLAFSCHLQSLANBELLSPDDSPFNIGDGTFTPKTSATTYSLTGDYF 60
QY 61 FYEPGCGTFLSDSCFCFQOTDNLTFLGNGHSLTFGFI DACTHGAASTTANKVLTFSGFS 120
| | | | |
DB 61 FYEPGCGTFLSDSCFCFQOTDNLTFLGNGHSLTFGFI DACTHGAASTTANKVLTFSGFS 120
QY 121 LLSFDSSEPTTYTGGGTSLSAGVNL ENIRKLVVAGNFSADGAIKAGSFLLTGTSGD 180
| | | | |
DB 121 LLSFDSSEPTTYTGGGTSLSAGVNL ENIRKLVVAGNFSADGAIKAGSFLLTGTSGD 180
QY 181 ALFSNNSSSTKGAIATTAGARIANTGYVRFLSNIASTSGAIDDEGTSILSNKFLYF 240
| | | | |
DB 181 ALFSNNSSSTKGAIATTAGARIANTGYVRFLSNIASTSGAIDDEGTSILSNKFLYF 240
QY 241 EGNAAKTGGAI CNTAASGSPELII SNKTLIFASVVAETSGAIIHAKKLALSSGGFTF 300
| | | | |
DB 241 EGNAAKTGGAI CNTAASGSPELII SNKTLIFASVVAETSGAIIHAKKLALSSGGFTF 300
QY 301 LRNNVSSATPKGAI SIDASGELS SAETGNITFVRNTLTTTGSTDPKRNAINISNGK 360
| | | | |
DB 301 LRNNVSSATPKGAI SIDASGELS SAETGNITFVRNTLTTTGSTDPKRNAINISNGK 360
QY 361 FTFLRAAKHNTIFFYDPITSEGTSSDVLKINNNSAGALNPYOGTILFSGETTLADELKVA 420
| | | | |
DB 361 FTFLRAAKHNTIFFYDPITSEGTSSDVLKINNNSAGALNPYOGTILFSGETTLADELKVA 420
QY 421 DNKSSFTOPVSLSGGKLLQKVTLESTFSQDASGLGMDGTTLLSTTAGSITTTNLG 480
| | | | |
DB 421 DNKSSFTOPVSLSGGKLLQKVTLESTFSQDASGLGMDGTTLLSTTAGSITTTNLG 480
QY 481 INVDSLGLKQPVSLTKAGSNKTVISGKMLIDIBGNYESHMFSDOLFSLLKITVDAD 540
| | | | |
DB 481 INVDSLGLKQPVSLTKAGSNKTVISGKMLIDIBGNYESHMFSDOLFSLLKITVDAD 540
QY 541 VDTNVDISSLIPVPAEDPNSYGFQOGOMVMTTDTATNTKEATATWTGTGVPSPERKS 600
| | | | |
DB 541 VDTNVDISSLIPVPAEDPNSYGFQOGOMVMTTDTATNTKEATATWTGTGVPSPERKS 600
```

QY 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDNRRKGFRTTSG 660  
DB 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDNRRKGFRTTSG 660  
QY 661 YVIGSAHTPKDDLFTPAFCHLPARDKCFIAHNSRTYGGTLFPKGSHTLQPNYLRIG 720  
DB 661 YVIGSAHTPKDDLFTPAFCHLPARDKCFIAHNSRTYGGTLFPKGSHTLQPNYLRIG 720  
QY 721 RAKFSSEAIKPREPLALDVQVFSHSDNMEHTYSLPESGSMNECIAAGIGL 780  
DB 721 RAKFSSEAIKPREPLALDVQVFSHSDNMEHTYSLPESGSMNECIAAGIGL 780  
QY 781 PVLSPHPLFKFTIPIOMKEMVYVSONSPFESSDGRGFSIGRLNLSIPYAKFVQGD 840  
DB 781 PVLSPHPLFKFTIPIOMKEMVYVSONSPFESSDGRGFSIGRLNLSIPYAKFVQGD 840  
QY 841 IGDSTYDLSGFFVSDVYNNPOSTATLVMSPDWIKIRGNLSROAFLRGSNYYNSN 900  
DB 841 IGDSTYDLSGFFVSDVYNNPOSTATLVMSPDWIKIRGNLSROAFLRGSNYYNSN 900  
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928  
DB 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928

## RESULT 3

US-10-289-762-478  
; Sequence 478, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention of infection and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 478  
; LENGTH: 949  
; TYPE: PRN  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: 1...949  
; OTHER INFORMATION: Xaa=unknown or other  
US-10-289-762-478

Query Match 89.1%; Score 827; DB 4; Length 949;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKTISPMVLVSVLAFCSHLOSLANBELSPDPSFNGNIDSGTFTPKTSATYSLTGDFV 60  
DB 22 MKTISPMVLVSVLAFCSHLOSLANBELSPDPSFNGNIDSGTFTPKTSATYSLTGDFV 81  
QY 61 FYEPGKGTPLSDSCFKOTTDNLTFLANGSLTRGFDAGTHAAGAASTTANKULTSNGFS 120  
DB 82 FYEPGKGTPLSDSCFKOTTDNLTFLANGSLTRGFDAGTHAAGAASTTANKULTSNGFS 141  
QY 121 LLSFDDSPSTVTYTGCGTSSAGVNLNRLVVGPNFTAGGAIKXGSPFLITGSGD 180  
DB 142 LLSFDDSPSTVTYTGCGTSSAGVNLNRLVVGPNFTAGGAIKXGSPFLITGSGD 201  
QY 181 ALFSNNSSSTKGAIAITTAGARIANNVYRFLSNIASTSGAIDDEGTSILSNKFLYF 240  
DB 202 ALFSNNSSSTKGAIAITTAGARIANNVYRFLSNIASTSGAIDDEGTSILSNKFLYF 261  
QY 241 EGNAAKTTGGAICNTYASGSPPELLISNNKTLIFASNAVAETSGAIIHAKKLALSSGGFTF 300  
DB 262 EGNAAKTTGGAICNTYASGSPPELLISNNKTLIFASNAVAETSGAIIHAKKLALSSGGFTF 321

QY 301 LRNNVSSATPKCGAISIDASGELSLSAETGNITPVARNLTITTTGSDTTPRRAINIGSNCK 360  
DB 322 LRNNVSSATPKCGAISIDASGELSLSAETGNITPVARNLTITTTGSDTTPRRAINIGSNCK 381  
QY 361 FTBLRAAKNHTIFPDPIITSEGTSSDVLKINNAGALNPYOGTILFSGETITLADBLKXA 420  
DB 382 FTBLRAAKNHTIFPDPIITSEGTSSDVLKINNAGALNPYOGTILFSGETITLADBLKXA 441  
QY 421 DNLKSFQTPVSLSGCKLLOKGVTLLESTSPQEAASLGMDSGTTLSTTAGSITTTNIG 480  
DB 442 DNLKSFQTPVSLSGCKLLOKGVTLLESTSPQEAASLGMDSGTTLSTTAGSITTTNIG 501  
QY 481 INVDSLGLKQPVSLTAKGANKVIVSGKLNLIIDEGNIESHMFSDQLFSLKITVDAD 540  
DB 502 INVDSLGLKQPVSLTAKGANKVIVSGKLNLIIDEGNIESHMFSDQLFSLKITVDAD 561  
QY 541 VDTNVDISLIVPAEDPNSSEYFGQGMVNMVTTDTATNTKATATWTTCGVSPERS 600  
DB 562 VDTNVDISLIVPAEDPNSSEYFGQGMVNMVTTDTATNTKATATWTTCGVSPERS 621  
QY 601 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDNRRKGFRTTSG 660  
DB 622 ALVCNTLMGVFTDIRSLQOLVEIGATGMEHKQGFVWSMTNPLHKTGDNRRKGFRTTSG 681  
QY 661 YVIGSAHTPKDDLFTPAFCHLPARDKCFIAHNSRTYGGTLFPKGSHTLQPNYLRIG 720  
DB 682 YVIGSAHTPKDDLFTPAFCHLPARDKCFIAHNSRTYGGTLFPKGSHTLQPNYLRIG 741  
QY 721 RAKFSSEAIKPREPLALDVQVFSHSDNMEHTYSLPESGSMNECIAAGIGL 780  
DB 742 RAKFSSEAIKPREPLALDVQVFSHSDNMEHTYSLPESGSMNECIAAGIGL 801  
QY 781 PVLSPHPLFKFTIPIOMKEMVYVSONSPFESSDGRGFSIGRLNLSIPYAKFVQGD 840  
DB 802 PVLSPHPLFKFTIPIOMKEMVYVSONSPFESSDGRGFSIGRLNLSIPYAKFVQGD 861  
QY 841 IGDSTYDLSGFFVSDVYNNPOSTATLVMSPDWIKIRGNLSROAFLRGSNYYNSN 900  
DB 862 IGDSTYDLSGFFVSDVYNNPOSTATLVMSPDWIKIRGNLSROAFLRGSNYYNSN 921  
QY 901 CELFGHYAMELRGSSRNRYNDVGTCLRF 928  
DB 922 CELFGHYAMELRGSSRNRYNDVGTCLRF 949

## RESULT 4

US-10-289-762-30  
; Sequence 30, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention of infection and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 30  
; LENGTH: 230  
; TYPE: PRN  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-30

Query Match 1.3%; Score 12; DB 4; Length 230;

Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;

QY 910 ELRGSSRNRYND 921  
DB 212 ELRGSSRNRYND 223

```
RESULT 5
; US-10-312-273-19
; Sequence 19, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 19
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-19

Query Match      1.3%; Score 12; DB 4; Length 746;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      910 ELRGSSRNRYND 921
Db      728 ELRGSSRNRYND 739

RESULT 6
; US-09-428-122-2
; Sequence 2, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 19721-007-019
; CURRENT APPLICATION NUMBER: US/09/428,122
; CURRENT FILING DATE: 1999-10-27
; EARLIER APPLICATION NUMBER: 60/106,046
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/132,271
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-428-122-2

Query Match      1.3%; Score 12; DB 3; Length 928;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      910 ELRGSSRNRYND 921
Db      910 ELRGSSRNRYND 921
```

```
Db      910 ELRGSSRNRYND 921

RESULT 7
; US-10-312-273-21
; Sequence 21, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035WO
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 21
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-21

Query Match      1.1%; Score 10; DB 4; Length 395;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      910 ELRGSSRNRYN 919
Db      377 ELRGSSRNRYN 386

RESULT 8
; US-10-289-762-35
; Sequence 35, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 35
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-35

Query Match      1.1%; Score 10; DB 4; Length 450;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      910 ELRGSSRNRYN 919
Db      432 ELRGSSRNRYN 441
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```
RESULT 9
US-09-738-269-23
; Sequence 23, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-09-738-269-23

Query Match
Best Local Similarity 100.0%; Score 10; DB 3; Length 839;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TDNLTFLGNG 88
DB 81 TDNLTFLGNG 90

RESULT 10
US-10-023-437-23
; Sequence 23, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS for Vaccination COMPRISING NUCLEIC ACID
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSD:736US
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-10-023-437-23

Query Match
Best Local Similarity 100.0%; Score 10; DB 4; Length 839;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 TDNLTFLGNG 88
DB 81 TDNLTFLGNG 90

RESULT 11
US-10-312-273-45
; Sequence 45, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
```

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FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312,273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWIn99, version 1.02
; SEQ ID NO 45
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-45

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 930;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AGAAASTTA 110
DB 107 AGAAASTTA 115

RESULT 12
US-10-289-762-470
; Sequence 470, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifflair, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 470
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-470

Query Match
Best Local Similarity 100.0%; Score 9; DB 4; Length 930;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AGAAASTTA 110
DB 107 AGAAASTTA 115

RESULT 13
US-10-282-122A-54680
; Sequence 54680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haseibeck, Robert
```

APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA 034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 54680  
LENGTH: 930  
TYPE: PRT  
ORGANISM: Chlamydia pneumoniae  
US-10-282-122A-54680

Query Match 1.0%; Score 9; DB 4; Length 930;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AGAASTTA 110  
DB 107 AGAASTTA 115

RESULT 14  
US-10-425-115-353071  
Sequence 353071, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 353071  
LENGTH: 53  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_85171C.1.pep  
US-10-425-115-353071

Query Match 0.9%; Score 8; DB 4; Length 53;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 TPKDULFT 676  
DB 42 TPKDULFT 49

RESULT 15  
US-10-617-320-3629  
Sequence 3629, Application US/10617320  
Publication No. US20050136404A1  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS  
THERAPEUTICS  
NUMBER OF SEQUENCES: 5206  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
City: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: <Unknown>  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: <Unknown>  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/617,320  
FILING DATE: 10-Jul-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,433  
FILING DATE: 30-Jun-1998  
APPLICATION NUMBER: 60/085131  
FILING DATE: May 12, 1998  
APPLICATION NUMBER: 60/051553  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 3629:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 76 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...76  
SEQUENCE DESCRIPTION: SEQ ID NO: 3629:  
US-10-617-320-3629

Query Match 0.9%; Score 8; DB 5; Length 76;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 412 LTADELKV 419  
DB 25 LTADELKV 32

Search completed: November 25, 2005, 14:56:26

Mon Nov 28 09:39:52 2005

us-09-446-677b-2.oli.rapbm

Page 7

Job time : 99.9541 secs

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GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: November 25, 2005, 14:37:47 ; Search time 3.58994 Seconds  
(without alignments)  
783.506 Million cell updates/sec

Title: US-09-446-677b-2  
Perfect score: 928  
Sequence: 1 MKTSLPWLVSVAFLAFSCHL.....MELRGSSRNVDVGTGRF 928

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 17545 seqs, 3030971 residues

Word size: 7

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_AA\_New:\*

1: /cgn2\_6/prodata/2/pubppa/US10\_NEW\_PUB pep: \*  
2: /cgn2\_6/prodata/2/pubppa/US06\_NEW\_PUB pep: \*  
3: /cgn2\_6/prodata/2/pubppa/US07\_NEW\_PUB pep: \*  
4: /cgn2\_6/prodata/2/pubppa/US08\_NEW\_PUB pep: \*  
5: /cgn2\_6/prodata/2/pubppa/US09\_NEW\_PUB pep: \*  
6: /cgn2\_6/prodata/2/pubppa/PCT\_NEW\_PUB pep: \*  
7: /cgn2\_6/prodata/2/pubppa/US11\_NEW\_PUB pep: \*  
8: /cgn2\_6/prodata/2/pubppa/US60\_NEW\_PUB pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                 | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1          | 7     | 0.8         | 245    | US-11-054-515-1714 | Sequence 1714, Ap  |
| 2          | 7     | 0.8         | 248    | US-11-054-515-895  | Sequence 895, App  |
| 3          | 7     | 0.8         | 249    | US-11-054-515-1142 | Sequence 1142, Ap  |
| 4          | 7     | 0.8         | 249    | US-11-054-515-1204 | Sequence 1204, Ap  |
| 5          | 7     | 0.8         | 249    | US-11-054-515-1205 | Sequence 1205, Ap  |
| 6          | 7     | 0.8         | 249    | US-11-054-515-1215 | Sequence 1215, Ap  |
| 7          | 7     | 0.8         | 250    | US-11-054-515-901  | Sequence 901, App  |
| 8          | 7     | 0.8         | 250    | US-11-054-515-1017 | Sequence 1017, App |
| 9          | 7     | 0.8         | 250    | US-11-054-515-1032 | Sequence 1032, Ap  |
| 10         | 7     | 0.8         | 250    | US-11-054-515-1158 | Sequence 1158, Ap  |
| 11         | 7     | 0.8         | 250    | US-11-054-515-1203 | Sequence 1203, App |
| 12         | 7     | 0.8         | 250    | US-11-054-515-1222 | Sequence 1222, Ap  |
| 13         | 7     | 0.8         | 250    | US-11-054-515-1228 | Sequence 1228, Ap  |
| 14         | 7     | 0.8         | 250    | US-11-054-515-1715 | Sequence 1715, Ap  |
| 15         | 7     | 0.8         | 251    | US-11-054-515-904  | Sequence 904, App  |
| 16         | 7     | 0.8         | 251    | US-11-054-515-1023 | Sequence 1023, Ap  |
| 17         | 7     | 0.8         | 251    | US-11-054-515-1133 | Sequence 1133, Ap  |
| 18         | 7     | 0.8         | 251    | US-11-054-515-1154 | Sequence 1154, Ap  |
| 19         | 7     | 0.8         | 251    | US-11-054-515-1213 | Sequence 1213, Ap  |
| 20         | 7     | 0.8         | 251    | US-11-054-515-1217 | Sequence 1217, Ap  |
| 21         | 7     | 0.8         | 251    | US-11-054-515-1225 | Sequence 1225, Ap  |
| 22         | 7     | 0.8         | 251    | US-11-054-515-1231 | Sequence 1231, Ap  |
| 23         | 7     | 0.8         | 251    | US-11-054-515-1487 | Sequence 1487, Ap  |
| 24         | 7     | 0.8         | 251    | US-11-054-515-1831 | Sequence 1831, Ap  |
| 25         | 7     | 0.8         | 252    | US-11-054-515-1144 | Sequence 1144, Ap  |

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|----|---|-----|------|--------------------|--------------------|
| 26 | 7 | 0.8 | 252  | US-11-054-515-1208 | Sequence 1208, Ap  |
| 27 | 7 | 0.8 | 253  | US-11-054-515-929  | Sequence 929, App  |
| 28 | 7 | 0.8 | 253  | US-11-054-515-935  | Sequence 935, App  |
| 29 | 7 | 0.8 | 253  | US-11-054-515-939  | Sequence 939, App  |
| 30 | 7 | 0.8 | 308  | US-10-793-626-1072 | Sequence 1072, Ap  |
| 31 | 7 | 0.8 | 308  | US-10-793-626-2706 | Sequence 2706, Ap  |
| 32 | 7 | 0.8 | 394  | US-10-793-626-3292 | Sequence 3292, Ap  |
| 33 | 7 | 0.8 | 417  | US-10-858-730-60   | Sequence 60, App   |
| 34 | 7 | 0.8 | 3144 | US-11-055-035-1    | Sequence 1, App1   |
| 35 | 6 | 0.6 | 16   | US-11-054-515-2907 | Sequence 2907, Ap  |
| 36 | 6 | 0.6 | 90   | US-11-053-076-146  | Sequence 146, App  |
| 37 | 6 | 0.6 | 92   | US-10-689-742-6    | Sequence 6, App1   |
| 38 | 6 | 0.6 | 92   | US-11-053-076-121  | Sequence 121, App1 |
| 39 | 6 | 0.6 | 124  | US-11-040-159-10   | Sequence 10, App1  |
| 40 | 6 | 0.6 | 142  | US-10-789-273-16   | Sequence 16, App1  |
| 41 | 6 | 0.6 | 142  | US-10-821-234-929  | Sequence 929, App  |
| 42 | 6 | 0.6 | 142  | US-10-821-234-1030 | Sequence 1030, Ap  |
| 43 | 6 | 0.6 | 144  | US-10-793-626-1640 | Sequence 1640, Ap  |
| 44 | 6 | 0.6 | 144  | US-10-793-626-1958 | Sequence 1958, Ap  |
| 45 | 6 | 0.6 | 144  | US-11-174-398-10   | Sequence 10, App1  |

## ALIGNMENTS

RESULT 1  
US-11-054-515-1714  
; Sequence 1714, Application US/11054515  
; Publication No. US2005025532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blus  
; FILE REFERENCE: PFS23P3  
; CURRENT APPLICATION NUMBER: US/11/054, 515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543, 296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580, 347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293, 418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331, 469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340, 817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880, 748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293, 499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277, 379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276, 248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240, 816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1714  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-1714  
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Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 411 TTAADEL 417  
DB 69 TTTAADEL 75  
RESULT 2

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US-11-054-515-895
; Sequence 895, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 895
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-895

Query Match      0.8%; Score 7; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      411 TLTDEL 417
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Db      68 TLTDEL 74

RESULT 3
US-11-054-515-1142
; Sequence 1142, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1204
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1204

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Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-11-054-515-1204
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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1142
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1142

Query Match      0.8%; Score 7; DB 7; Length 249;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      411 TLTDEL 417
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Db      68 TLTDEL 74

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US-11-054-515-1204
; Sequence 1204, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1204
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1204

Query Match      0.8%; Score 7; DB 7; Length 249;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      411 TLTDEL 417
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Db      69 TLTDEL 75

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US-11-054-515-1205
; Sequence 1205, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1205
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1205
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Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      411 TTAADEL 417
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Db       69 TTTAADEL 75
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US-11-054-515-1215
; Sequence 1215, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
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; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
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; SEQ ID NO 1215
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1215
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Best Local Similarity 100.0%; Pred. No. 7.5;
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Db       69 TTTAADEL 75
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; Publication No. US2005025532A1
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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; NUMBER OF SEQ ID NOS: 3247
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; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-901
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Best Local Similarity 100.0%; Pred. No. 7.5;
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QY      411 TTAADEL 417
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Db       69 TTTAADEL 75
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US-11-054-515-1017
; Sequence 1017, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
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; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1017
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1017
```

Query Match 0.8%; Score 7; DB 7; Length 250;

Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;

```
Oy 411 TLTADL 417
    |||||
Db 69 TLTADL 75
```

```
RESULT 9
US-11-054-515-1022
; Sequence 1022, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1022
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1022
```

Query Match 0.8%; Score 7; DB 7; Length 250;

```
Oy 411 TLTADL 417
    |||||
Db 69 TLTADL 75
```

```
RESULT 10
US-11-054-515-1158
; Sequence 1158, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1158
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1158

Query Match 0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 411 TLTADL 417
    |||||
Db 69 TLTADL 75

RESULT 11
US-11-054-515-1203
; Sequence 1203, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
```



```

; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1203
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1203
```

```

Query Match      0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      411 TLTADEL 417
Db      69 TLTADEL 75
```

```

RESULT 12
US-11-054-515-1222
; Sequence 1222, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1222
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1222
```

```

Query Match      0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      411 TLTADEL 417
Db      69 TLTADEL 75
```

```

RESULT 13
US-11-054-515-1228
; Sequence 1228, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1228
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1228
```

```

Query Match      0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      411 TLTADEL 417
Db      69 TLTADEL 75
```

```

RESULT 14
US-11-054-515-1715
; Sequence 1715, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
```

Search completed: November 25, 2005, 14:56:47  
Job time : 4.83994 secs

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; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1715
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1715

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```

Query Match      0.8%; Score 7; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      411 TLTADEL 417
Db      69 TLTADEL 75

```

```

RESULT 15
US-11-054-515-904
; Sequence 904, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 904
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-904

```

```

Query Match      0.8%; Score 7; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      411 TLTADEL 417
Db      69 TLTADEL 75

```

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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